

SEQUENCE LISTING

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Maurer, Patrick
Lechner, Franziska
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<120> Molecular Antigen Array

<130> 1700.0190004

<140> (To be assigned)
<141> 2002-01-18

<150> US 60/262,379
<151> 2001-01-19

<150> US 60/288,549
<151> 2001-05-04

<150> US 60/326,998
<151> 2001-10-05

<150> US 60/331,045
<151> 2001-11-07

<160> 350

<170> PatentIn Ver. 2.1

<210> 1
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<223> Description of Artificial Sequence: Primer

<400> 1
ggggacgcgt gcagcaggta accaccgtta aagaaggcac c

41

<210> 2
<211> 44
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<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 2
cggtgggttac ctgctgcacg cggttgcttaa gcgacatgta gcgg

44

<210> 3
<211> 20
<212> DNA
<213> Artificial Sequence

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<220>
 <223> Description of Artificial Sequence: Primer

<400> 3
 ccatgaggcc tacgataccc 20

<210> 4
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 4
 ggcactcacg gcgcgcttta caggc 25

<210> 5
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 5
 cttctcttaa cgggtggttac ctgctggcaa ccaacgtggt tcatgac 47

<210> 6
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 <212> DNA
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<220>
 <223> Description of Artificial Sequence: Primer

<400> 6
 aagcatgctg cacgcgtgtg cgggtggctcg atcgcccggc 40

<210> 7
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 7
 gggctctagat tcccaaccat tcccttatcc aggctttttg acaacgctat gctccgcgcc 60
 catcgtctgc accagctggc ctttgacacc 90

<210> 8
 <211> 108
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

10050902 "01.1302

<400> 8
gggtctagaa ggaggtaaaa aacgatgaaa aagacagcta tcgcgattgc agtggcactg 60
gctggtttcg ctaccgtagc gcaggccttc ccaaccattc cttatcc 108

<210> 9
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 9
cccgaattcc tagaagccac agctgccctc c 31

<210> 10
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 10
cctgcggtgg tctgaccgac accc 24

<210> 11
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 11
ccgcggaaga gccaccgcaa ccaccgtgtg ccgccaggat g 41

<210> 12
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 12
ctatcatcta gaatgaatag aggattcttt aac 33

<210> 13
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Modified ribosome
binding site

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<400> 13
aggaggtaaa aaacg

15

<210> 14
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: signal peptide

<400> 14
Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala Gly Phe Ala
1 5 10 15
Thr Val Ala Gln Ala
20

<210> 15
<211> 46
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: modified Fos
construct

<400> 15
Cys Gly Gly Leu Thr Asp Thr Leu Gln Ala Glu Thr Asp Gln Val Glu
1 5 10 15
Asp Glu Lys Ser Ala Leu Gln Thr Glu Ile Ala Asn Leu Leu Lys Glu
20 25 30
Lys Glu Lys Leu Glu Phe Ile Leu Ala Ala His Gly Gly Cys
35 40 45

<210> 16
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: peptide linker

<400> 16
Ala Ala Ala Ser Gly Gly
1 5

<210> 17
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: peptide linker

<400> 17
Gly Gly Ser Ala Ala Ala

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1

5

<210> 18
<211> 256
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fos fusion construct

<400> 18
gaattcagga ggtaaaaaac gatgaaaaag acagctatcg cgattgcagt ggcactggct 60
ggtttcgcta ccgtagcgca ggcctgggtg ggggcggccg cttctgggtg ttgcggtggt 120
ctgaccgaca ccctgcaggc ggaaaccgac caggtggaag acgaaaaatc cgcgctgcaa 180
accgaaatcg cgaacctgct gaaagaaaaa gaaaagctgg agttcatcct ggcggcacac 240
ggtggttgct aagctt 256

<210> 19
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fos fusion construct

<400> 19
Ala Ala Ala Ser Gly Gly Cys Gly Gly Leu Thr Asp Thr Leu Gln Ala
5 10 15
Glu Thr Asp Gln Val Glu Asp Glu Lys Ser Ala Leu Gln Thr Glu Ile
20 25 30
Ala Asn Leu Leu Lys Glu Lys Glu Lys Leu Glu Phe Ile Leu Ala Ala
35 40 45
His Gly Gly Cys
50

<210> 20
<211> 261
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fos fusion construct

<220>
<221> CDS
<222> (22)..(240)

<400> 20
gaattcagga ggtaaaaaac g atg aaa aag aca gct atc gcg att gca gtg 51
Met Lys Lys Thr Ala Ile Ala Ile Ala Val
1 5 10
gca ctg gct ggt ttc gct acc gta gcg cag gcc tgc ggt ggt ctg acc 99
Ala Leu Ala Gly Phe Ala Thr Val Ala Gln Ala Cys Gly Gly Leu Thr
15 20 25

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gac acc ctg cag gcg gaa acc gac cag gtg gaa gac gaa aaa tcc gcg 147
 Asp Thr Leu Gln Ala Glu Thr Asp Gln Val Glu Asp Glu Lys Ser Ala
 30 35 40

ctg caa acc gaa atc gcg aac ctg ctg aaa gaa aaa gaa aag ctg gag 195
 Leu Gln Thr Glu Ile Ala Asn Leu Leu Lys Glu Lys Glu Lys Leu Glu
 45 50 55

ttc atc ctg gcg gca cac ggt ggt tgc ggt ggt tct gcg gcc gct 240
 Phe Ile Leu Ala Ala His Gly Gly Cys Gly Gly Ser Ala Ala Ala
 60 65 70

gggtgtgggg atatcaagct t 261

<210> 21
 <211> 73
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Fos fusion
 construct

<400> 21
 Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala Gly Phe Ala
 1 5 10 15

Thr Val Ala Gln Ala Cys Gly Gly Leu Thr Asp Thr Leu Gln Ala Glu
 20 25 30

Thr Asp Gln Val Glu Asp Glu Lys Ser Ala Leu Gln Thr Glu Ile Ala
 35 40 45

Asn Leu Leu Lys Glu Lys Glu Lys Leu Glu Phe Ile Leu Ala Ala His
 50 55 60

Gly Gly Cys Gly Gly Ser Ala Ala Ala
 65 70

<210> 22
 <211> 196
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Fos fusion
 construct

<220>
 <221> CDS
 <222> (34)..(189)

<400> 22
 gaattcagga ggtaaaaaga tatcgggtgt ggg gcg gcc gct tct ggt ggt tgc 54
 Ala Ala Ala Ser Gly Gly Cys
 1 5

ggt ggt ctg acc gac acc ctg cag gcg gaa acc gac cag gtg gaa gac 102
 Gly Gly Leu Thr Asp Thr Leu Gln Ala Glu Thr Asp Gln Val Glu Asp
 10 15 20

20050502 0130E

gaa aaa tcc gcg ctg caa acc gaa atc gcg aac ctg ctg aaa gaa aaa 150
 Glu Lys Ser Ala Leu Gln Thr Glu Ile Ala Asn Leu Leu Lys Glu Lys
 25 30 35

gaa aag ctg gag ttc atc ctg gcg gca cac ggt ggt tgc taagctt 196
 Glu Lys Leu Glu Phe Ile Leu Ala Ala His Gly Gly Cys
 40 45 50

<210> 23
 <211> 52
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Fos fusion
 construct

<400> 23
 Ala Ala Ala Ser Gly Gly Cys Gly Gly Leu Thr Asp Thr Leu Gln Ala
 1 5 10 15
 Glu Thr Asp Gln Val Glu Asp Glu Lys Ser Ala Leu Gln Thr Glu Ile
 20 25 30
 Ala Asn Leu Leu Lys Glu Lys Glu Lys Leu Glu Phe Ile Leu Ala Ala
 35 40 45
 His Gly Gly Cys
 50

<210> 24
 <211> 204
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Fos fusion
 construct

<400> 24
 gaattcagga ggtaaaaaac gatggcttgc ggtgggtctga cgcacaccct gcaggcgga 60
 accgaccagg tggaagacga aaaatccgcg ctgcaaaccg aaatcgcgaa cctgctgaaa 120
 gaaaaagaaa agctggagtt catcctggcg gcacacgggtg gttgcgggtg ttctgcggcc 180
 gctgggtgtg gggatatcaa gctt 204

<210> 25
 <211> 56
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Fos fusion
 construct

<400> 25
 Lys Thr Met Ala Cys Gly Gly Leu Thr Asp Thr Leu Gln Ala Glu Thr
 1 5 10 15
 Asp Gln Val Glu Asp Glu Lys Ser Ala Leu Gln Thr Glu Ile Ala Asn

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20 25 30
 Leu Leu Lys Glu Lys Glu Lys Leu Glu Phe Ile Leu Ala Ala His Gly
 35 40 45
 Gly Cys Gly Gly Ser Ala Ala Ala
 50 55

<210> 26
 <211> 26
 <212> PRT
 <213> Homo sapiens

<400> 26
 Met Ala Thr Gly Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly Leu Leu
 1 5 10 15

Cys Leu Pro Trp Leu Gln Glu Gly Ser Ala
 20 25

<210> 27
 <211> 262
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Fos fusion
 construct

<400> 27
 gaattcaggc ctatggctac aggctcccgg acgtccctgc tcctggcttt tggcctgctc 60
 tgcctgccct ggcttcaaga gggcagcgct ggggtgtggg cggccgcttc tgggtggtgc 120
 ggtggtctga cgcacaccct gcaggcggaa accgaccagg tggaagacga aaaatccgcg 180
 ctgcaaaccg aaatcgcgaa cctgctgaaa gaaaaagaaa agctggagtt catcctggcg 240
 gcacacgggtg gttgctaagc tt 262

<210> 28
 <211> 52
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Fos fusion
 construct

<400> 28
 Ala Ala Ala Ser Gly Gly Cys Gly Gly Leu Thr Asp Thr Leu Gln Ala
 5 10 15

Glu Thr Asp Gln Val Glu Asp Glu Lys Ser Ala Leu Gln Thr Glu Ile
 20 25 30

Ala Asn Leu Leu Lys Glu Lys Glu Lys Leu Glu Phe Ile Leu Ala Ala
 35 40 45

His Gly Gly Cys
 50

<210> 29

10050500.01302

<211> 261
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fos fusion
construct

<220>
<221> CDS
<222> (7)..(240)

<400> 29
gaattc atg gct aca ggc tcc cgg acg tcc ctg ctc ctg gct ttt ggc 48
Met Ala Thr Gly Ser Arg Thr Ser Leu Leu Ala Phe Gly
1 5 10
ctg ctc tgc ctg ccc tgg ctt caa gag ggc agc gct tgc ggt ggt ctg 96
Leu Leu Cys Leu Pro Trp Leu Gln Glu Gly Ser Ala Cys Gly Gly Leu
15 20 25 30
acc gac acc ctg cag gcg gaa acc gac cag gtg gaa gac gaa aaa tcc 144
Thr Asp Thr Leu Gln Ala Glu Thr Asp Gln Val Glu Asp Glu Lys Ser
35 40 45
gcg ctg caa acc gaa atc gcg aac ctg ctg aaa gaa aaa gaa aag ctg 192
Ala Leu Gln Thr Glu Ile Ala Asn Leu Leu Lys Glu Lys Glu Lys Leu
50 55 60
gag ttc atc ctg gcg gca cac ggt ggt tgc ggt ggt tct gcg gcc gct 240
Glu Phe Ile Leu Ala Ala His Gly Gly Cys Gly Gly Ser Ala Ala Ala
65 70 75
gggtgtggga ggcctaagct t 261

<210> 30
<211> 78
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fos fusion
construct

<400> 30
Met Ala Thr Gly Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly Leu Leu
1 5 10 15
Cys Leu Pro Trp Leu Gln Glu Gly Ser Ala Cys Gly Gly Leu Thr Asp
20 25 30
Thr Leu Gln Ala Glu Thr Asp Gln Val Glu Asp Glu Lys Ser Ala Leu
35 40 45
Gln Thr Glu Ile Ala Asn Leu Leu Lys Glu Lys Glu Lys Leu Glu Phe
50 55 60
Ile Leu Ala Ala His Gly Gly Cys Gly Gly Ser Ala Ala Ala
65 70 75

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<210> 31
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 31
cctgggtggg ggcggccgct tctggtggtt gcggtggtct gacc 44

<210> 32
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 32
ggtgggaatt caggaggtaa aaagatatcg ggtgtggggc ggcc 44

<210> 33
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 33
ggtgggaatt caggaggtaa aaaacgatgg cttgcggtgg tctgacc 47

<210> 34
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 34
gcttgcggtg gtctgacc 18

<210> 35
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 35
ccaccaagct tagcaaccac cgtgtgc 27

<210> 36
<211> 54
<212> DNA

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<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 36

ccaccaagct tgatatcccc acaccagcg gccgcagaac caccgcaacc accg

54

<210> 37

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 37

ccaccaagct taggcctccc acaccagcg gc

32

<210> 38

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 38

ggtgggaatt caggaggtaa aaaacgatg

29

<210> 39

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 39

ggtgggaatt caggcctatg gctacaggct cc

32

<210> 40

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 40

ggtgggaatt catggctaca ggctccc

27

<210> 41

<211> 59

<212> DNA

<213> Artificial Sequence

<220>

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<223> Description of Artificial Sequence: Primer

<400> 41
gggtctagaa tggctacagg ctcccgacg tccctgctcc tggcttttgg cctgctctg 59

<210> 42
<211> 58
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 42
cgcaggcctc ggcaactgccc tcttgaagcc agggcaggca gagcaggcca aaagccag 58

<210> 43
<211> 402
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Modified bee
venom phospholipase A2

<220>
<221> CDS
<222> (1)..(402)

<400> 43
atc atc tac cca ggt act ctg tgg tgt ggt cac ggc aac aaa tct tct 48
Ile Ile Tyr Pro Gly Thr Leu Trp Cys Gly His Gly Asn Lys Ser Ser
1 5 10 15

ggt ccg aac gaa ctc ggc cgc ttt aaa cac acc gac gca tgc tgt cgc 96
Gly Pro Asn Glu Leu Gly Arg Phe Lys His Thr Asp Ala Cys Cys Arg
20 25 30

acc cag gac atg tgt ccg gac gtc atg tct gct ggt gaa tct aaa cac 144
Thr Gln Asp Met Cys Pro Asp Val Met Ser Ala Gly Glu Ser Lys His
35 40 45

ggg tta act aac acc gct tct cac acg cgt ctc agc tgc gac tgc gac 192
Gly Leu Thr Asn Thr Ala Ser His Thr Arg Leu Ser Cys Asp Cys Asp
50 55 60

gac aaa ttc tac gac tgc ctt aag aac tcc gcc gat acc atc tct tct 240
Asp Lys Phe Tyr Asp Cys Leu Lys Asn Ser Ala Asp Thr Ile Ser Ser
65 70 75 80

tac ttc gtt ggt aaa atg tat ttc aac ctg atc gat acc aaa tgt tac 288
Tyr Phe Val Gly Lys Met Tyr Phe Asn Leu Ile Asp Thr Lys Cys Tyr
85 90 95

aaa ctg gaa cac ccg gta acc ggc tgc ggc gaa cgt acc gaa ggt cgc 336
Lys Leu Glu His Pro Val Thr Gly Cys Gly Glu Arg Thr Glu Gly Arg
100 105 110

tgc ctg cac tac acc gtt gac aaa tct aaa ccg aaa gtt tac cag tgg 384
Cys Leu His Tyr Thr Val Asp Lys Ser Lys Pro Lys Val Tyr Gln Trp
115 120 125

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ttc gac ctg cgc aaa tac
Phe Asp Leu Arg Lys Tyr
130

402

<210> 44
<211> 134
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Modified bee
venom phospholipase A2

<400> 44
Ile Ile Tyr Pro Gly Thr Leu Trp Cys Gly His Gly Asn Lys Ser Ser
1 5 10 15
Gly Pro Asn Glu Leu Gly Arg Phe Lys His Thr Asp Ala Cys Cys Arg
20 25 30
Thr Gln Asp Met Cys Pro Asp Val Met Ser Ala Gly Glu Ser Lys His
35 40 45
Gly Leu Thr Asn Thr Ala Ser His Thr Arg Leu Ser Cys Asp Cys Asp
50 55 60
Asp Lys Phe Tyr Asp Cys Leu Lys Asn Ser Ala Asp Thr Ile Ser Ser
65 70 75 80
Tyr Phe Val Gly Lys Met Tyr Phe Asn Leu Ile Asp Thr Lys Cys Tyr
85 90 95
Lys Leu Glu His Pro Val Thr Gly Cys Gly Glu Arg Thr Glu Gly Arg
100 105 110
Cys Leu His Tyr Thr Val Asp Lys Ser Lys Pro Lys Val Tyr Gln Trp
115 120 125
Phe Asp Leu Arg Lys Tyr
130

<210> 45
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 45
ccatcatcta cccaggtac

19

<210> 46
<211> 34
<212> DNA
<213> Artificial Sequence

<220>

208TTT-01802

<223> Description of Artificial Sequence: Primer

<400> 46
cccacacca gcggccgcgt atttgcgag gtcg 34

<210> 47
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 47
cgggtggttct gcggccgcta tcattctaccc aggtac 36

<210> 48
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 48
ttagtatttg cgcaggtcg 19

<210> 49
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 49
ccggctccat cgggtgcag 18

<210> 50
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 50
accaccagaa gcggccgcag gggaaacaca tctgcc 36

<210> 51
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 51

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cggtggttct gcggccgctg gctccatcgg tgcag 35

<210> 52
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 52
ttaaggggaa acacatctgc c 21

<210> 53
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 53
actagtctag aatgagagtg aaggagaaat atc 33

<210> 54
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 54
tagcatgcta gcaccgaatt tatctaattc caataattct tg 42

<210> 55
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 55
gtagcaccca ccaaggcaaa gctgaaagct acccagctcg agaaactggc a 51

<210> 56
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 56
caaagctcct attcccactg ccagtttctc gagctgggta gctttcag 48

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<210> 57
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 57
 ttcggtgcta gcggtggctg cgggtgtctg accgac 36

<210> 58
 <211> 37
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 58
 gatgctgggc ccttaaccgc aaccaccgtg tgccgcc 37

<210> 59
 <211> 46
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: JUN amino acid
 sequence

<400> 59
 Cys Gly Gly Arg Ile Ala Arg Leu Glu Glu Lys Val Lys Thr Leu Lys
 1 5 10 15
 Ala Gln Asn Ser Glu Leu Ala Ser Thr Ala Asn Met Leu Arg Glu Gln
 20 25 30
 Val Ala Gln Leu Lys Gln Lys Val Met Asn His Val Gly Cys
 35 40 45

<210> 60
 <211> 46
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: FOS amino
 acid sequence

<400> 60
 Cys Gly Gly Leu Thr Asp Thr Leu Gln Ala Glu Thr Asp Gln Val Glu
 1 5 10 15
 Asp Glu Lys Ser Ala Leu Gln Thr Glu Ile Ala Asn Leu Leu Lys Glu
 20 25 30
 Lys Glu Lys Leu Glu Phe Ile Leu Ala Ala His Gly Gly Cys
 35 40 45

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<210> 61
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 61
ccggaattca tgtgcggtgg tcggatcgcc cgg 33

<210> 62
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 62
gtcgcgtaccc gcggctccgc aaccaacgtg gttcatgac 39

<210> 63
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 63
gttggttgcg gagccgcggg tagcgacatt gacccttata aagaatttgg 50

<210> 64
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 64
cgcgtcccaa gcttctacgg aagcgttgat aggatagg 38

<210> 65
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 65
ctagccgcgg gttgcggtgg tcggatcgcc cgg 33

<210> 66
<211> 38
<212> DNA

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<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 66

cgcggtcccaa gcttttagca accaacgtgg ttcattgac

38

<210> 67

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 67

ccggaattca tggacattga cccttataaa g

31

<210> 68

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 68

ccgaccaccg caaccgcggg ctagcggaag cggtgatagg atagg

45

<210> 69

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 69

ctaattgatc cggtgggggc tgcggtgggc ggatcgcccg gctcgag

47

<210> 70

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 70

gtcgctaccc ggggctccgc aaccaacgtg gttcatgac

39

<210> 71

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

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<223> Description of Artificial Sequence: Primer

<400> 71
ccggaattca tggacattga cccttataaa g 31

<210> 72
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 72
ccgaccaccg cagccccac cggatccatt agtaccacc caggtagc 48

<210> 73
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 73
gttggttgcg gagccgcggg tagcgaccta gtagtcagtt atgtc 45

<210> 74
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 74
cgcgccccaa gcttctacgg aagcgttgat aggatagg 38

<210> 75
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 75
ctagccgcgg gttgcggtgg tcggatcgcc cgg 33

<210> 76
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 76

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cgcggtcccaa gcttttagca accaacgtgg ttcattgac 38

<210> 77
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 77
ccggaattca tggccacact tttaaggagc 30

<210> 78
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 78
cgcggtcccaa gcttttagca accaacgtgg ttcattgac 38

<210> 79
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 79
ccggaattca tggacattga cccttataaa g 31

<210> 80
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 80
cctagagcca cctttgccac catcttctaa attagtagcc acccaggtag c 51

<210> 81
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 81
gaagatgggtg gcaaagggtg ctctaggagc ctagtagtca gttatgtc 48

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<210> 82
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 82
cgcggtcccaa gcttctaaac aacagtagtc tccggaag 38

<210> 83
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 83
gccgaattcc tagcagctag caccgaattt atctaa 36

<210> 84
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 84
ggttaagtcg acatgagagt gaaggagaaa tat 33

<210> 85
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 85
taaccgaatt caggaggtaa aaagatatgg 30

<210> 86
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 86
gaagtaaagc ttttaaccac cgcaaccacc agaag 35

<210> 87
<211> 33
<212> DNA

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<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 87

tcgaatgggc cctcatcttc gtgtgctagt cag

33

<210> 88

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fos fusion construct

<400> 88

Glu Phe Arg Arg

1

<210> 89

<211> 183

<212> PRT

<213> Hepatitis B virus

<400> 89

Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
1 5 10 15

Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
20 25 30

Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
35 40 45

Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu
50 55 60

Leu Met Thr Leu Ala Thr Trp Val Gly Gly Asn Leu Glu Asp Pro Ile
65 70 75 80

Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys
85 90 95

Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
100 105 110

Glu Thr Val Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
115 120 125

Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
130 135 140

Glu Thr Thr Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr
145 150 155 160

Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser
165 170 175

Gln Ser Arg Gly Ser Gln Cys

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180

<210> 90
 <211> 183
 <212> PRT
 <213> Hepatitis B virus

<400> 90
 Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
 1 5 10 15
 Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
 20 25 30
 Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
 35 40 45
 Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu
 50 55 60
 Leu Met Thr Leu Ala Thr Trp Val Gly Gly Asn Leu Glu Asp Pro Thr
 65 70 75 80
 Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys
 85 90 95
 Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
 100 105 110
 Glu Thr Val Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
 115 120 125
 Pro Pro Ala Tyr Arg Pro Thr Asn Ala Pro Ile Leu Ser Thr Leu Pro
 130 135 140
 Glu Thr Cys Val Ile Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr
 145 150 155 160
 Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser
 165 170 175
 Gln Ser Arg Gly Ser Gln Cys
 180

<210> 91
 <211> 212
 <212> PRT
 <213> Hepatitis B virus

<400> 91
 Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
 1 5 10 15
 Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
 20 25 30
 Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
 35 40 45
 Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
 50 55 60

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Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65 70 75 80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr
85 90 95

Leu Ala Thr Trp Val Gly Gly Asn Leu Glu Asp Pro Ile Ser Arg Asp
100 105 110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
115 120 125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
130 135 140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145 150 155 160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
165 170 175

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
180 185 190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
195 200 205

Glu Ser Gln Cys
210

<210> 92
<211> 212
<212> PRT
<213> Hepatitis B virus

<400> 92
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1 5 10 15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
20 25 30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
35 40 45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Asn Ala Ser
50 55 60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65 70 75 80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr
85 90 95

Leu Ala Thr Trp Val Gly Gly Asn Leu Glu Asp Pro Ile Ser Arg Asp
100 105 110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
115 120 125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
130 135 140

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Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
 145 150 155 160
 Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
 165 170 175
 Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
 180 185 190
 Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
 195 200 205
 Glu Ser Gln Cys
 210

<210> 93
 <211> 183
 <212> PRT
 <213> Hepatitis B virus

<400> 93
 Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
 1 5 10 15
 Ser Phe Leu Pro Thr Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
 20 25 30
 Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
 35 40 45
 Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu
 50 55 60
 Leu Met Thr Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala
 65 70 75 80
 Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys
 85 90 95
 Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
 100 105 110
 Glu Thr Val Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
 115 120 125
 Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
 130 135 140
 Glu Thr Cys Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr
 145 150 155 160
 Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser
 165 170 175
 Gln Ser Arg Glu Ser Gln Cys
 180

<210> 94
 <211> 212
 <212> PRT
 <213> Hepatitis B virus

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<400> 94

Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
 1 5 10 15
 Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
 20 25 30
 Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
 35 40 45
 Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
 50 55 60
 Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
 65 70 75 80
 His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Asp Leu Met Thr
 85 90 95
 Leu Ala Thr Trp Val Gly Gly Asn Leu Glu Asp Pro Val Ser Arg Asp
 100 105 110
 Leu Val Val Ser Tyr Val Asn Thr Asn Val Gly Leu Lys Phe Arg Gln
 115 120 125
 Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
 130 135 140
 Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
 145 150 155 160
 Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
 165 170 175
 Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
 180 185 190
 Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
 195 200 205
 Glu Ser Gln Cys
 210

<210> 95

<211> 212

<212> PRT

<213> Hepatitis B virus

<400> 95

Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
 1 5 10 15
 Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Asp Met Asp Ile
 20 25 30
 Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
 35 40 45
 Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
 50 55 60

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Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65 70 75 80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Asp Leu Met Thr
85 90 95

Leu Ala Thr Trp Val Gly Gly Asn Leu Glu Asp Pro Val Ser Arg Asp
100 105 110

Leu Val Val Ser Tyr Val Asn Thr Asn Val Gly Leu Lys Phe Arg Gln
115 120 125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
130 135 140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145 150 155 160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
165 170 175

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
180 185 190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
195 200 205

Glu Ser Gln Cys
210

<210> 96
<211> 212
<212> PRT
<213> Hepatitis B virus

<400> 96
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1 5 10 15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
20 25 30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
35 40 45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
50 55 60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro Gln
65 70 75 80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr
85 90 95

Leu Ala Thr Trp Val Gly Gly Asn Leu Glu Asp Pro Ile Ser Arg Asp
100 105 110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
115 120 125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
130 135 140

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Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
 145 150 155 160
 Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
 165 170 175
 Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
 180 185 190
 Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
 195 200 205
 Glu Ser Gln Cys
 210

<210> 97
 <211> 212
 <212> PRT
 <213> Hepatitis B virus

<400> 97
 Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
 1 5 10 15
 Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
 20 25 30
 Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
 35 40 45
 Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
 50 55 60
 Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
 65 70 75 80
 His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr
 85 90 95
 Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp
 100 105 110
 Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
 115 120 125
 Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
 130 135 140
 Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
 145 150 155 160
 Tyr Lys Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
 165 170 175
 Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
 180 185 190
 Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
 195 200 205
 Gly Ser Gln Cys
 210

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<210> 98
 <211> 183
 <212> PRT
 <213> Hepatitis B virus

<400> 98
 Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
 1 5 10 15
 Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
 20 25 30
 Thr Ala Ser Ala Leu Phe Arg Asp Ala Leu Glu Ser Pro Glu His Cys
 35 40 45
 Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu
 50 55 60
 Leu Met Thr Leu Ala Thr Trp Val Gly Gly Asn Leu Glu Asp Pro Ala
 65 70 75 80
 Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys
 85 90 95
 Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
 100 105 110
 Asp Thr Val Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
 115 120 125
 Pro Pro Ala Tyr Arg Pro Ser Asn Ala Pro Ile Leu Ser Thr Leu Pro
 130 135 140
 Glu Thr Cys Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr
 145 150 155 160
 Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser
 165 170 175
 Gln Ser Arg Glu Ser Gln Cys
 180

<210> 99
 <211> 183
 <212> PRT
 <213> Hepatitis B virus

<400> 99
 Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
 1 5 10 15
 Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
 20 25 30
 Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
 35 40 45
 Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu
 50 55 60

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Leu Met Thr Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala
65 70 75 80

Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys
85 90 95

Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
100 105 110

Glu Thr Val Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
115 120 125

Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
130 135 140

Glu Thr Thr Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr
145 150 155 160

Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser
165 170 175

Gln Ser Arg Glu Ser Gln Cys
180

<210> 100
<211> 212
<212> PRT
<213> Hepatitis B virus

<400> 100
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1 5 10 15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
20 25 30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
35 40 45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
50 55 60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65 70 75 80

His Thr Ala Leu Arg His Ala Ile Leu Cys Trp Gly Asp Leu Arg Thr
85 90 95

Leu Ala Thr Trp Val Gly Gly Asn Leu Glu Asp Pro Ile Ser Arg Asp
100 105 110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
115 120 125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
130 135 140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145 150 155 160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
165 170 175

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Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
180 185 190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
195 200 205

Glu Ser Gln Cys
210

<210> 101

<211> 212

<212> PRT

<213> Hepatitis B virus

<400> 101

Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1 5 10 15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Asp Met Asp Ile
20 25 30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
35 40 45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
50 55 60

Ala Leu Phe Arg Asp Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65 70 75 80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr
85 90 95

Leu Ala Thr Trp Val Gly Ala Asn Leu Glu Asp Pro Ala Ser Arg Asp
100 105 110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
115 120 125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
130 135 140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Gln Ala
145 150 155 160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Cys
165 170 175

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
180 185 190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
195 200 205

Glu Ser Gln Cys
210

<210> 102

<211> 183

<212> PRT

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<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic human Hepatitis B construct

<400> 102

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Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
 1           5           10           15

Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
          20           25           30
Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
          35           40           45

Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu
          50           55           60

Leu Met Thr Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala
 65           70           75           80

Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys
          85           90           95

Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
          100           105           110

Glu Thr Val Leu Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
          115           120           125

Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
          130           135           140

Glu Thr Thr Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr
          145           150           155           160

Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser
          165           170           175

Gln Ser Arg Glu Ser Gln Cys
          180

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<210> 103

<211> 212

<212> PRT

<213> Hepatitis B virus

<400> 103

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Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
 1           5           10           15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
          20           25           30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
          35           40           45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
          50           55           60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
          65           70           75           80

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His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Asp Leu Met Ser
85 90 95

Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ile Ser Arg Asp
100 105 110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
115 120 125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
130 135 140
Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145 150 155 160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
165 170 175

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
180 185 190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
195 200 205

Glu Ser Gln Cys
210

<210> 104

<211> 183

<212> PRT

<213> Hepatitis B virus

<400> 104

Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
1 5 10 15

Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
20 25 30

Thr Ala Ser Ala Leu Tyr Arg Asp Ala Leu Glu Ser Pro Glu His Cys
35 40 45

Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu
50 55 60

Leu Met Thr Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala
65 70 75 80

Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys
85 90 95

Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
100 105 110

Glu Thr Val Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
115 120 125

Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
130 135 140

Glu Thr Thr Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr
145 150 155 160

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Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser
165 170 175

Gln Ser Arg Glu Ser Gln Cys
180

<210> 105

<211> 183

<212> PRT

<213> Hepatitis B virus

<400> 105

Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
1 5 10 15

Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
20 25 30

Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
35 40 45

Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Asp
50 55 60

Leu Met Thr Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala
65 70 75 80

Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys
85 90 95

Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
100 105 110

Glu Thr Val Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
115 120 125

Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
130 135 140

Glu Thr Thr Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr
145 150 155 160

Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser
165 170 175

Gln Ser Arg Glu Ser Gln Cys
180

<210> 106

<211> 183

<212> PRT

<213> Hepatitis B virus

<400> 106

Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
1 5 10 15

Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
20 25 30

Thr Ala Ser Ala Leu Tyr Arg Asp Ala Leu Glu Ser Pro Glu His Cys

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35	40	45
Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu		
50	55	60
Leu Met Thr Leu Ala Thr Trp Val Gly Ala Asn Leu Glu Asp Pro Ala		
65	70	75
Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys		
	85	90
Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg		
	100	105
Glu Thr Val Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr		
	115	120
Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro		
	130	135
Glu Thr Thr Val Val Arg Arg Gly Arg Thr Pro Arg Arg Arg Thr		
145	150	155
Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser		
	165	170
Gln Ser Arg Glu Ser Gln Cys		
	180	

<210> 107
 <211> 212
 <212> PRT
 <213> Hepatitis B virus

<400> 107
 Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
 1 5 10 15
 Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
 20 25 30
 Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
 35 40 45
 Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
 50 55 60
 Ala Leu Tyr Arg Asp Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
 65 70 75 80
 His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr
 85 90 95
 Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp
 100 105 110
 Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
 115 120 125
 Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
 130 135 140

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Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145 150 155 160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
165 170 175

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
180 185 190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
195 200 205

Glu Ser Gln Cys
210

<210> 108
<211> 212
<212> PRT
<213> Hepatitis B virus

<400> 108
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1 5 10 15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
20 25 30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
35 40 45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
50 55 60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65 70 75 80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Asp Leu Met Thr
85 90 95

Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp
100 105 110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
115 120 125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
130 135 140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145 150 155 160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
165 170 175

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
180 185 190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
195 200 205

Glu Ser Gln Cys
210

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<210> 109
 <211> 212
 <212> PRT
 <213> Hepatitis B virus

<400> 109
 Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Thr Cys Pro Thr
 1 5 10 15
 Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
 20 25 30
 Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
 35 40 45
 Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
 50 55 60
 Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
 65 70 75 80
 His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr
 85 90 95
 Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp
 100 105 110
 Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
 115 120 125
 Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
 130 135 140
 Ile Glu Tyr Leu Val Ala Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
 145 150 155 160
 Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
 165 170 175
 Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
 180 185 190
 Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
 195 200 205
 Glu Ser Gln Cys
 210

<210> 110
 <211> 212
 <212> PRT
 <213> Hepatitis B virus

<400> 110
 Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
 1 5 10 15
 Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
 20 25 30

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Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
35 40 45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
50 55 60

Ala Leu Tyr Arg Glu Ala Phe Glu Cys Ser Glu His Cys Ser Pro His
65 70 75 80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr
85 90 95

Leu Ala Thr Trp Val Gly Gly Asn Leu Glu Asp Pro Ile Ser Arg Asp
100 105 110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
115 120 125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
130 135 140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145 150 155 160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
165 170 175

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
180 185 190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
195 200 205

Glu Ser Gln Cys
210

<210> 111
<211> 212
<212> PRT
<213> Hepatitis B virus

<220>
<221> UNSURE
<222> (28)
<223> May be any amino acid.

<400> 111
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1 5 10 15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Xaa Asp Met Asp Ile
20 25 30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
35 40 45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
50 55 60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65 70 75 80

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His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Asp Leu Ile Thr
85 90 95

Leu Ser Thr Trp Val Gly Gly Asn Leu Glu Asp Pro Thr Ser Arg Asp
100 105 110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
115 120 125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
130 135 140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145 150 155 160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
165 170 175

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
180 185 190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Thr Gln Ser Arg
195 200 205

Glu Ser Gln Cys
210

<210> 112
<211> 212
<212> PRT
<213> Hepatitis B virus

<400> 112
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1 5 10 15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
20 25 30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
35 40 45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Asn Ala Ser
50 55 60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65 70 75 80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr
85 90 95

Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp
100 105 110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
115 120 125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
130 135 140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145 150 155 160

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Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
 165 170 175
 Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
 180 185 190
 Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
 195 200 205
 Glu Ser Gln Cys
 210

<210> 113
 <211> 212
 <212> PRT
 <213> Hepatitis B virus

<400> 113
 Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
 1 5 10 15
 Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
 20 25 30
 Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
 35 40 45
 Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
 50 55 60
 Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
 65 70 75 80
 His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr
 85 90 95
 Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp
 100 105 110
 Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
 115 120 125
 Leu Leu Trp Phe His Ile Cys Cys Leu Thr Phe Gly Arg Glu Thr Val
 130 135 140
 Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
 145 150 155 160
 Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
 165 170 175
 Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
 180 185 190
 Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
 195 200 205
 Glu Ser Gln Cys
 210

<210> 114

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<211> 212
<212> PRT
<213> Hepatitis B virus

<400> 114
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1 5 10 15
Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
20 25 30
Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
35 40 45
Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
50 55 60
Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65 70 75 80
His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr
85 90 95
Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp
100 105 110
Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
115 120 125
Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
130 135 140
Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145 150 155 160
Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
165 170 175
Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
180 185 190
Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
195 200 205
Glu Pro Gln Cys
210

<210> 115
<211> 212
<212> PRT
<213> Hepatitis B virus

<400> 115
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1 5 10 15
Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
20 25 30
Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
35 40 45

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Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Ser Thr Ala Ser
50 55 60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65 70 75 80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr
85 90 95

Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp
100 105 110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
115 120 125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
130 135 140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145 150 155 160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
165 170 175

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
180 185 190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
195 200 205

Glu Ser Gln Cys
210

<210> 116
<211> 212
<212> PRT
<213> Hepatitis B virus

<400> 116
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1 5 10 15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
20 25 30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
35 40 45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
50 55 60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65 70 75 80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr
85 90 95

Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp
100 105 110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
115 120 125

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Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
 130 135 140
 Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
 145 150 155 160
 Tyr Arg Pro Pro Asn Ala Pro Ile Leu Leu Thr Leu Pro Glu Thr Thr
 165 170 175
 Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
 180 185 190
 Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
 195 200 205
 Glu Ser Gln Cys
 210

<210> 117
 <211> 212
 <212> PRT
 <213> Hepatitis B virus

<400> 117
 Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
 1 5 10 15
 Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
 20 25 30
 Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
 35 40 45
 Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
 50 55 60
 Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
 65 70 75 80
 His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Asp Leu Met Thr
 85 90 95
 Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp
 100 105 110
 Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Lys Gln
 115 120 125
 Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
 130 135 140
 Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
 145 150 155 160
 Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
 165 170 175
 Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
 180 185 190
 Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
 195 200 205

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Glu Ser Gln Cys
210

<210> 118
<211> 212
<212> PRT
<213> Hepatitis B virus

<400> 118
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1 5 10 15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
20 25 30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
35 40 45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ala
50 55 60

Ala Leu Tyr Arg Asp Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65 70 75 80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr
85 90 95

Leu Ala Thr Trp Val Gly Thr Asn Leu Glu Asp Pro Ala Ser Arg Asp
100 105 110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
115 120 125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
130 135 140

Leu Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145 150 155 160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
165 170 175

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
180 185 190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
195 200 205

Glu Ser Gln Cys
210

<210> 119
<211> 183
<212> PRT
<213> Hepatitis B virus

<400> 119
Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Ser Met Glu Leu Leu
1 5 10 15

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Ser Phe Leu Pro Ser Asp Phe Tyr Pro Ser Val Arg Asp Leu Leu Asp
20 25 30

Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
35 40 45

Thr Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu
50 55 60

Leu Met Thr Leu Ala Thr Trp Val Gly Gly Asn Leu Gln Asp Pro Thr
65 70 75 80

Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys
85 90 95

Phe Arg Gln Leu Leu Trp Phe His Val Ser Cys Leu Thr Phe Gly Arg
100 105 110

Glu Thr Val Val Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
115 120 125

Pro Gln Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
130 135 140

Glu Thr Cys Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr
145 150 155 160

Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Ser
165 170 175

Gln Ser Arg Glu Ser Gln Cys
180

<210> 120
<211> 183
<212> PRT
<213> Hepatitis B virus

<400> 120
Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
1 5 10 15

Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
20 25 30

Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
35 40 45

Ser Pro His His Thr Ala Leu Arg His Val Phe Leu Cys Trp Gly Asp
50 55 60

Leu Met Thr Leu Ala Thr Trp Val Gly Gly Asn Leu Glu Asp Pro Thr
65 70 75 80

Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys
85 90 95

Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
100 105 110

Glu Thr Val Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
115 120 125

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Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
 130 135 140
 Glu Thr Thr Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr
 145 150 155 160
 Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser
 165 170 175
 Gln Ser Arg Glu Ser Gln Cys
 180

<210> 121
 <211> 212
 <212> PRT
 <213> Hepatitis B virus

<400> 121
 Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
 1 5 10 15
 Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
 20 25 30
 Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
 35 40 45
 Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
 50 55 60
 Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
 65 70 75 80
 His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Asp Leu Thr Thr
 85 90 95
 Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp
 100 105 110
 Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
 115 120 125
 Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
 130 135 140
 Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
 145 150 155 160
 Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
 165 170 175
 Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
 180 185 190
 Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
 195 200 205
 Glu Ser Gln Cys
 210

<210> 122

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<211> 212
<212> PRT
<213> Hepatitis B virus

<400> 122
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1 5 10 15
Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
20 25 30
Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
35 40 45
Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
50 55 60
Ala Leu Tyr Arg Asp Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65 70 75 80
His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr
85 90 95
Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp
100 105 110
Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
115 120 125
Leu Leu Trp Phe His Ile Ser Cys Leu Ile Phe Gly Arg Glu Thr Val
130 135 140
Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145 150 155 160
Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
165 170 175
Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
180 185 190
Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
195 200 205
Glu Ser Gln Cys
210

<210> 123
<211> 183
<212> PRT
<213> Hepatitis B virus

<400> 123
Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
1 5 10 15
Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
20 25 30
Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
35 40 45

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Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Asp
50 55 60

Leu Met Thr Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Val
65 70 75 80

Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Val Gly Leu Lys
85 90 95

Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
100 105 110

Glu Thr Val Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
115 120 125

Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
130 135 140

Glu Thr Thr Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr
145 150 155 160

Pro Ser Pro Ala Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser
165 170 175

Gln Ser Arg Glu Ser Gln Cys
180

<210> 124
<211> 212
<212> PRT
<213> Hepatitis B virus

<400> 124
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1 5 10 15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
20 25 30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
35 40 45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
50 55 60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65 70 75 80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Asp Leu Met Asn
85 90 95

Leu Ala Thr Trp Val Gly Gly Asn Leu Glu Asp Pro Val Ser Arg Asp
100 105 110

Leu Val Val Gly Tyr Val Asn Thr Thr Val Gly Leu Lys Phe Arg Gln
115 120 125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
130 135 140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145 150 155 160

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Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
 165 170 175
 Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
 180 185 190
 Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
 195 200 205
 Glu Ser Gln Cys
 210

<210> 125
 <211> 183
 <212> PRT
 <213> Hepatitis B virus

<400> 125
 Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
 1 5 10 15
 Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
 20 25 30
 Thr Ala Ser Ala Leu Tyr Arg Asp Ala Leu Glu Ser Pro Glu His Cys
 35 40 45
 Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Asp
 50 55 60
 Leu Met Thr Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala
 65 70 75 80
 Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys
 85 90 95
 Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
 100 105 110
 Glu Thr Val Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
 115 120 125
 Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
 130 135 140
 Glu Thr Thr Val Val Arg Arg Arg Gly Arg Thr Pro Arg Arg Arg Thr
 145 150 155 160
 Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser
 165 170 175
 Gln Ser Arg Glu Ser Gln Cys
 180

<210> 126
 <211> 212
 <212> PRT
 <213> Hepatitis B virus

<400> 126
 Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr

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1	5	10	15
Val Gln Ala Ser 20	Lys Leu Cys Leu 25	Gly Trp Leu Trp 30	Gly Met Asp Ile
Asp Pro Tyr 35	Lys Glu Phe Gly 40	Ala Thr Val Glu Leu 45	Leu Ser Phe Leu
Pro Ser Asp 50	Phe Phe Pro Ser 55	Val Arg Ala Leu 60	Leu Asp Thr Ala Ser
Ala Leu Tyr Arg 65	Glu Ala Leu Glu 70	Ser Pro Glu His 75	Cys Ser Pro His 80
His Thr Ala Leu 85	Arg Gln Ala Ile Leu 90	Cys Trp Gly Glu Leu 95	Met Thr
Leu Ala Thr 100	Trp Val Gly Val Asn 105	Leu Glu Asp Pro Ala 110	Ser Arg Asp
Leu Val Val 115	Ser Tyr Val Asn Thr 120	Asn Met Gly Leu Lys 125	Phe Arg Gln
Ile Leu Trp 130	Phe His Ile Ser 135	Cys Leu Thr Phe Gly 140	Arg Glu Thr Val
Ile Glu Tyr Leu 145	Val Ser Phe Gly Val Trp 150	Ile Arg Thr Pro Pro 155	Ala 160
Tyr Arg Pro Pro 165	Asn Ala Pro Ile Leu Ser 170	Thr Leu Pro Glu Thr Thr 175	
Val Val Arg Arg 180	Arg Gly Arg Ser Pro 185	Arg Arg Arg Thr Pro 190	Ser Pro
Arg Arg Arg Arg 195	Ser Gln Ser Pro 200	Arg Arg Arg Ser 205	Gln Ser Arg
Glu Ser Gln Cys 210			

<210> 127
 <211> 212
 <212> PRT
 <213> Hepatitis B virus

<400> 127
 Met Gln Leu Phe His 5 Leu Cys Leu Ile Ile 10 Ser Cys Ser Cys Pro Thr 15
 Val Gln Ala Ser 20 Lys Leu Cys Leu Gly 25 Trp Leu Trp Gly Met Asp Ile 30
 Asp Pro Tyr 35 Lys Glu Phe Gly 40 Ala Thr Val Glu Leu Leu 45 Ser Phe Leu
 Pro Ser Asp 50 Phe Phe Pro Ser 55 Val Arg Asp Leu Leu 60 Asp Thr Ala Ser
 Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His 80
 65 70 75

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His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Asp Leu Met Thr
85 90 95

Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Thr Arg Asp
100 105 110

Leu Val Val Ser Tyr Val Asn Thr Asn Val Gly Leu Lys Phe Arg Gln
115 120 125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
130 135 140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145 150 155 160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
165 170 175

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
180 185 190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
195 200 205

Glu Ser Gln Cys
210

<210> 128
<211> 212
<212> PRT
<213> Hepatitis B virus

<400> 128
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1 5 10 15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
20 25 30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
35 40 45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
50 55 60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65 70 75 80

His Thr Ala Leu Arg Gln Arg Ile Leu Cys Trp Gly Glu Leu Met Thr
85 90 95

Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp
100 105 110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
115 120 125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
130 135 140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145 150 155 160

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Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
165 170 175

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
180 185 190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Thr Arg Ser Gln Ser Arg
195 200 205

Glu Ser Gln Cys
210

<210> 129

<211> 212

<212> PRT

<213> Hepatitis B virus

<400> 129

Met Gln Leu Phe His Leu Cys Leu Val Ile Ser Cys Ser Cys Pro Thr
1 5 10 15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
20 25 30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
35 40 45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ala
50 55 60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65 70 75 80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr
85 90 95

Leu Ala Thr Trp Val Gly Asn Asn Leu Glu Asp Pro Ala Ser Arg Asp
100 105 110

Leu Val Val Asn Tyr Val Asn Thr Asn Met Gly Leu Lys Ile Arg Gln
115 120 125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
130 135 140

Leu Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145 150 155 160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
165 170 175

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
180 185 190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
195 200 205

Glu Ser Gln Cys
210

<210> 130

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<211> 212
<212> PRT
<213> Hepatitis B virus

<400> 130
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1 5 10 15
Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
20 25 30
Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
35 40 45
Pro Ser Ala Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
50 55 60
Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65 70 75 80
His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Asp Leu Met Thr
85 90 95
Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp
100 105 110
Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
115 120 125
Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
130 135 140
Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145 150 155 160
Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
165 170 175
Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
180 185 190
Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
195 200 205
Glu Ser Gln Cys
210

<210> 131
<211> 183
<212> PRT
<213> Hepatitis B virus

<400> 131
Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
1 5 10 15
Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
20 25 30
Thr Ala Ala Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
35 40 45

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Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu
50 55 60

Leu Met Thr Leu Ala Thr Trp Val Gly Asn Asn Leu Glu Asp Pro Ala
65 70 75 80

Ser Arg Asp Leu Val Val Asn Tyr Val Asn Thr Asn Met Gly Leu Lys
85 90 95

Ile Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
100 105 110

Glu Thr Val Leu Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
115 120 125

Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
130 135 140

Glu Thr Thr Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr
145 150 155 160

Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser
165 170 175

Gln Ser Arg Glu Ser Gln Cys
180

<210> 132
<211> 183
<212> PRT
<213> Hepatitis B virus

<400> 132
Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
1 5 10 15

Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
20 25 30

Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
35 40 45

Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu
50 55 60

Leu Met Thr Leu Ala Thr Trp Val Gly Gly Asn Leu Glu Asp Pro Ile
65 70 75 80

Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys
85 90 95

Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
100 105 110

Glu Thr Val Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
115 120 125

Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
130 135 140

Glu Thr Cys Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr
145 150 155 160

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Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser
165 170 175

Gln Ser Arg Gly Ser Gln Cys
180

<210> 133
<211> 3221
<212> DNA
<213> Hepatitis B virus

<220>
<221> CDS
<222> (1901)..(2458)

<400> 133
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aatctccgcg aggactgggg accctgtgac gaacatggag aacatcacat caggattcct 180
aggacccctg ctctgtgttac aggcgggggtt ttattgttg acaagaatcc tcacaatacc 240
gcagagtcta gactcgtggg ggacttctct caattttata gggggatcac ccgtgtgtct 300
tggccaaaat tcgcagtcct caacctccaa tctctacca acctcctgtc ctccaatttg 360
tcttggttat cgctggatgt gtctgcggcg ttttatcata ttctcttca tctgtctgtc 420
atgcctcatc ttcttattgg ttcttctgga ttatcaaggt atgttgcccg tttgtcctct 480
aattccagga tcaacaacaa ccagtacggg accatgcaaa acctgcacga ctctgtctca 540
aggcaactct atgtttcct catgttgctg taaaaacct acggttgga attgcacctg 600
tattcccatc ccatcgtcct gggttttcgc aaaataccta tgggagtggg cctcagtcctg 660
tttctcttgg ctcatgttac tagtgccatt tgttcagtgg ttcgtagggc tttccccac 720
tgtttggtt tcagctatat ggatgatgtg gtattggggg ccaagtctgt acagcatcgt 780
gagtccttt ataccgctgt taccaatttt cttttgtctc tgggtataca tttaaaccct 840
aacaaaacaa aaagatgggg ttattcccta aacttcatgg gttacataat tggaagttgg 900
ggaacattgc cacaggatca tattgtacaa aagatcaaac actgttttag aaaacttcct 960
gttaacaggc ctattgattg gaaagtatgt caaagaattg tgggtctttt gggcttttgc 1020
gtccattta cacaatgtgg atatcctgcc ttaatgcctt tgtatgcatg tatacaggct 1080
aaacaggctt tctctttctc gccaaactac aaggcctttc taagtaaaca gtacatgaac 1140
ctttaccccg ttgctcggca acggcctggg ctgtgccaa tggttgctga cgcaaccccc 1200
actggttggg gcttggccat aggccatcag cgcagtgatg gaacctttgt ggctcctctg 1260
ccgatccata ctgcggaact cctagccgct tgtattgtct gcagccggtc tggagcaaag 1320
ctcatcgga ctgacaattc tgctgtcctc tcgcggaaat atacatcgtt tccatggctg 1380

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ctaggctgta	ctgccaactg	gataccttcgc	gggacgtcct	ttgtttacgt	cccgtcggcg	1440
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ctgccgttcc	agccgaccac	ggggcgcacc	tctctttacg	cggtctcccc	gtctgtgect	1560
tctcatctgc	cggtccgtgt	gcacttcgct	tcacctctgc	acgttgcatg	gagaccaccg	1620
tgaacgcccc	tcagatcctg	cccaaggtct	tacataagag	gactcttgga	ctcccagcaa	1680
tgtcaacgac	cgaccttgag	gcctacttca	aagactgtgt	gtttaaggac	tgggaggagc	1740
tggggggagga	gattagggtta	aaggtccttg	tattaggagg	ctgtaggcat	aaattggtct	1800
gcgcaccagc	accatgcaac	tttttcacct	ctgcctaata	atctcttgta	catgtcccac	1860
tgttcaagcc	tccaagctgt	gccttgggtg	gctttggggc	atg gac att gac cct		1915
				Met Asp Ile Asp Pro		
				1 5		
tat aaa gaa ttt gga gct act gtg gag tta ctc tcg ttt ttg cct tct						1963
Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Ser Phe Leu Pro Ser						
	10		15		20	
gac ttc ttt cct tcc gtc aga gat ctc cta gac acc gcc tca gct ctg						2011
Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser Ala Leu						
	25		30		35	
tat cga gaa gcc tta gag tct cct gag cat tgc tca cct cac cat act						2059
Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His His Thr						
	40		45		50	
gca ctc agg caa gcc att ctc tgc tgg ggg gaa ttg atg act cta gct						2107
Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr Leu Ala						
	55		60		65	
acc tgg gtg ggt aat aat ttg gaa gat cca gca tcc agg gat cta gta						2155
Thr Trp Val Gly Asn Asn Leu Glu Asp Pro Ala Ser Arg Asp Leu Val						
	70		75		80	85
gtc aat tat gtt aat act aac atg ggt tta aag atc agg caa cta ttg						2203
Val Asn Tyr Val Asn Thr Asn Met Gly Leu Lys Ile Arg Gln Leu Leu						
	90		95		100	
tgg ttt cat ata tct tgc ctt act ttt gga aga gag act gta ctt gaa						2251
Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val Leu Glu						
	105		110		115	
tat ttg gtc tct ttc gga gtg tgg att cgc act cct cca gcc tat aga						2299
Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala Tyr Arg						
	120		125		130	
cca cca aat gcc cct atc tta tca aca ctt ccg gaa act act gtt gtt						2347
Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr Val Val						
	135		140		145	
aga cga cgg gac cga ggc agg tcc cct aga aga aga act ccc tcg cct						2395
Arg Arg Arg Asp Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro						
	150		155		160	165
cgc aga cgc aga tct caa tcg ccg cgt cgc aga aga tct caa tct cgg						2443
Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg						
	170		175		180	

gaa tct caa tgt tag tattccttgg actcataagg tgggaaactt tactgggctt 2498
Glu Ser Gln Cys
185

tattcctcta cagtacctat cttaaatcct gaatggcaaa ctccttcctt tcctaagatt 2558
catttacaag aggacattat tgataggtgt caacaatttg tgggccctct cactgtaaatt 2618
gaaaagagaa gattgaaatt aattatgcct gctagattct atcctacca cactaaatat 2678
ttgcccttag acaaaggaat taaaccttat tatccagatc aggtagttaa tcattacttc 2738
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acacgtagcg catcattttg cgggtcacca tattcttggg aacaagagct acagcatggg 2858
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gggcatattg accacagtgt caacaattcc tcctcctgcc tccaccaatc ggcagtcagg 3158
aaggcagcct actcccatct ctccacctct aagagacagt catcctcagg ccatgcagtg 3218
gaa 3221

<210> 134
<211> 185
<212> PRT
<213> Hepatitis B virus

<400> 134
Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
1 5 10 15
Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
20 25 30
Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
35 40 45
Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu
50 55 60
Leu Met Thr Leu Ala Thr Trp Val Gly Asn Asn Leu Glu Asp Pro Ala
65 70 75 80
Ser Arg Asp Leu Val Val Asn Tyr Val Asn Thr Asn Met Gly Leu Lys
85 90 95
Ile Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
100 105 110
Glu Thr Val Leu Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
115 120 125
Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
130 135 140
Glu Thr Thr Val Val Arg Arg Arg Asp Arg Gly Arg Ser Pro Arg Arg
145 150 155 160
Arg Thr Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg
165 170 175
Arg Ser Gln Ser Arg Glu Ser Gln Cys
180 185

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<210> 135
 <211> 188
 <212> PRT
 <213> Woodchuck hepatitis B virus

<400> 135
 Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ser Ser Tyr Gln Leu Leu
 1 5 10 15
 Asn Phe Leu Pro Leu Asp Phe Phe Pro Asp Leu Asn Ala Leu Val Asp
 20 25 30
 Thr Ala Thr Ala Leu Tyr Glu Glu Glu Leu Thr Gly Arg Glu His Cys
 35 40 45
 Ser Pro His His Thr Ala Ile Arg Gln Ala Leu Val Cys Trp Asp Glu
 50 55 60
 Leu Thr Lys Leu Ile Ala Trp Met Ser Ser Asn Ile Thr Ser Glu Gln
 65 70 75 80
 Val Arg Thr Ile Ile Val Asn His Val Asn Asp Thr Trp Gly Leu Lys
 85 90 95
 Val Arg Gln Ser Leu Trp Phe His Leu Ser Cys Leu Thr Phe Gly Gln
 100 105 110
 His Thr Val Gln Glu Phe Leu Val Ser Phe Gly Val Trp Ile Arg Thr
 115 120 125
 Pro Ala Pro Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
 130 135 140
 Glu His Thr Val Ile Arg Arg Arg Gly Gly Ala Arg Ala Ser Arg Ser
 145 150 155 160
 Pro Arg Arg Arg Thr Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro
 165 170 175
 Arg Arg Arg Arg Ser Gln Ser Pro Ser Thr Asn Cys
 180 185

<210> 136
 <211> 217
 <212> PRT
 <213> Ground squirrel hepatitis virus

<400> 136
 Met Tyr Leu Phe His Leu Cys Leu Val Phe Ala Cys Val Pro Cys Pro
 1 5 10 15
 Thr Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Asp Met Asp
 20 25 30
 Ile Asp Pro Tyr Lys Glu Phe Gly Ser Ser Tyr Gln Leu Leu Asn Phe
 35 40 45
 Leu Pro Leu Asp Phe Phe Pro Asp Leu Asn Ala Leu Val Asp Thr Ala
 50 55 60
 Ala Ala Leu Tyr Glu Glu Glu Leu Thr Gly Arg Glu His Cys Ser Pro
 65 70 75 80

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His His Thr Ala Ile Arg Gln Ala Leu Val Cys Trp Glu Glu Leu Thr
85 90 95

Arg Leu Ile Thr Trp Met Ser Glu Asn Thr Thr Glu Glu Val Arg Arg
100 105 110

Ile Ile Val Asp His Val Asn Asn Thr Trp Gly Leu Lys Val Arg Gln
115 120 125

Thr Leu Trp Phe His Leu Ser Cys Leu Thr Phe Gly Gln His Thr Val
130 135 140

Gln Glu Phe Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Ala Pro
145 150 155 160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu His Thr
165 170 175

Val Ile Arg Arg Arg Gly Gly Ser Arg Ala Ala Arg Ser Pro Arg Arg
180 185 190

Arg Thr Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg
195 200 205

Arg Ser Gln Ser Pro Ala Ser Asn Cys
210 215

<210> 137
<211> 262
<212> PRT
<213> Snow Goose Hepatitis B Virus

<400> 137
Met Asp Val Asn Ala Ser Arg Ala Leu Ala Asn Val Tyr Asp Leu Pro
1 5 10 15

Asp Asp Phe Phe Pro Lys Ile Glu Asp Leu Val Arg Asp Ala Lys Asp
20 25 30

Ala Leu Glu Pro Tyr Trp Lys Ser Asp Ser Ile Lys Lys His Val Leu
35 40 45

Ile Ala Thr His Phe Val Asp Leu Ile Glu Asp Phe Trp Gln Thr Thr
50 55 60

Gln Gly Met His Glu Ile Ala Glu Ala Ile Arg Ala Val Ile Pro Pro
65 70 75 80

Thr Thr Ala Pro Val Pro Ser Gly Tyr Leu Ile Gln His Asp Glu Ala
85 90 95

Glu Glu Ile Pro Leu Gly Asp Leu Phe Lys Glu Gln Glu Glu Arg Ile
100 105 110

Val Ser Phe Gln Pro Asp Tyr Pro Ile Thr Ala Arg Ile His Ala His
115 120 125

Leu Lys Ala Tyr Ala Lys Ile Asn Glu Glu Ser Leu Asp Arg Ala Arg
130 135 140

Arg Leu Leu Trp Trp His Tyr Asn Cys Leu Leu Trp Gly Glu Ala Thr
145 150 155 160

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Val Thr Asn Tyr Ile Ser Arg Leu Arg Thr Trp Leu Ser Thr Pro Glu
165 170 175

Lys Tyr Arg Gly Arg Asp Ala Pro Thr Ile Glu Ala Ile Thr Arg Pro
180 185 190

Ile Gln Val Ala Gln Gly Gly Arg Lys Thr Ser Thr Ala Thr Arg Lys
195 200 205

Pro Arg Gly Leu Glu Pro Arg Arg Arg Lys Val Lys Thr Thr Val Val
210 215 220

Tyr Gly Arg Arg Arg Ser Lys Ser Arg Glu Arg Arg Ala Ser Ser Pro
225 230 235 240

Gln Arg Ala Gly Ser Pro Leu Pro Arg Ser Ser Ser Ser His His Arg
245 250 255

Ser Pro Ser Pro Arg Lys
260

<210> 138
<211> 305
<212> PRT
<213> Duck hepatitis B virus

<400> 138
Met Trp Asp Leu Arg Leu His Pro Ser Pro Phe Gly Ala Ala Cys Gln
1 5 10 15

Gly Ile Phe Thr Ser Ser Leu Leu Leu Phe Leu Val Thr Val Pro Leu
20 25 30

Val Cys Thr Ile Val Tyr Asp Ser Cys Leu Cys Met Asp Ile Asn Ala
35 40 45

Ser Arg Ala Leu Ala Asn Val Tyr Asp Leu Pro Asp Asp Phe Phe Pro
50 55 60

Lys Ile Asp Asp Leu Val Arg Asp Ala Lys Asp Ala Leu Glu Pro Tyr
65 70 75 80

Trp Arg Asn Asp Ser Ile Lys Lys His Val Leu Ile Ala Thr His Phe
85 90 95

Val Asp Leu Ile Glu Asp Phe Trp Gln Thr Thr Gln Gly Met His Glu
100 105 110

Ile Ala Glu Ala Leu Arg Ala Ile Ile Pro Ala Thr Thr Ala Pro Val
115 120 125

Pro Gln Gly Phe Leu Val Gln His Glu Glu Ala Glu Glu Ile Pro Leu
130 135 140

Gly Glu Leu Phe Arg Tyr Gln Glu Glu Arg Leu Thr Asn Phe Gln Pro
145 150 155 160

Asp Tyr Pro Val Thr Ala Arg Ile His Ala His Leu Lys Ala Tyr Ala
165 170 175

Lys Ile Asn Glu Glu Ser Leu Asp Arg Ala Arg Arg Leu Leu Trp Trp
180 185 190

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His Tyr Asn Cys Leu Leu Trp Gly Glu Pro Asn Val Thr Asn Tyr Ile
195 200 205

Ser Arg Leu Arg Thr Trp Leu Ser Thr Pro Glu Lys Tyr Arg Gly Lys
210 215 220

Asp Ala Pro Thr Ile Glu Ala Ile Thr Arg Pro Ile Gln Val Ala Gln
225 230 235 240

Gly Gly Arg Asn Lys Thr Gln Gly Val Arg Lys Ser Arg Gly Leu Glu
245 250 255

Pro Arg Arg Arg Arg Val Lys Thr Thr Ile Val Tyr Gly Arg Arg Arg
260 265 270

Ser Lys Ser Arg Glu Arg Arg Ala Pro Thr Pro Gln Arg Ala Gly Ser
275 280 285

Pro Leu Pro Arg Thr Ser Arg Asp His His Arg Ser Pro Ser Pro Arg
290 295 300

Glu
305

<210> 139
<211> 212
<212> PRT
<213> Haemophilus influenzae

<400> 139
Met Lys Lys Thr Leu Leu Gly Ser Leu Ile Leu Leu Ala Phe Ala Gly
1 5 10 15

Asn Val Gln Ala Ala Ala Asn Ala Asp Thr Ser Gly Thr Val Thr Phe
20 25 30

Phe Gly Lys Val Val Glu Asn Thr Cys Gln Val Asn Gln Asp Ser Glu
35 40 45

Tyr Glu Cys Asn Leu Asn Asp Val Gly Lys Asn His Leu Ser Gln Gln
50 55 60

Gly Tyr Thr Ala Met Gln Thr Pro Phe Thr Ile Thr Leu Glu Asn Cys
65 70 75 80

Asn Val Thr Thr Thr Asn Asn Lys Pro Lys Ala Thr Lys Val Gly Val
85 90 95

Tyr Phe Tyr Ser Trp Glu Ile Ala Asp Lys Asp Asn Lys Tyr Thr Leu
100 105 110

Lys Asn Ile Lys Glu Asn Thr Gly Thr Asn Asp Ser Ala Asn Lys Val
115 120 125

Asn Ile Gln Leu Leu Glu Asp Asn Gly Thr Ala Glu Ile Lys Val Val
130 135 140

Gly Lys Thr Thr Thr Asp Phe Thr Ser Glu Asn His Asn Gly Ala Gly
145 150 155 160

Ala Asp Pro Val Ala Thr Asn Lys His Ile Ser Ser Leu Thr Pro Leu
165 170 175

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Asn Asn Gln Asn Ser Ile Asn Leu His Tyr Ile Ala Gln Tyr Tyr Ala
 180 185 190
 Thr Gly Val Ala Glu Ala Gly Lys Val Pro Ser Ser Val Asn Ser Gln
 195 200 205
 Ile Ala Tyr Glu
 210

<210> 140
 <211> 139
 <212> PRT
 <213> Pseudomonas stutzeri

<400> 140
 Met Lys Ala Gln Met Gln Lys Gly Phe Thr Leu Ile Glu Leu Met Ile
 1 5 10 15
 Val Val Ala Ile Ile Gly Ile Leu Ala Ala Ile Ala Leu Pro Ala Tyr
 20 25 30
 Gln Asp Tyr Thr Val Arg Ser Asn Ala Ala Ala Ala Leu Ala Glu Ile
 35 40 45
 Thr Pro Gly Lys Ile Gly Phe Glu Gln Ala Ile Asn Glu Gly Lys Thr
 50 55 60
 Pro Ser Leu Thr Ser Thr Asp Glu Gly Tyr Ile Gly Ile Thr Asp Ser
 65 70 75 80
 Thr Ser Tyr Cys Asp Val Asp Leu Asp Thr Ala Ala Asp Gly His Ile
 85 90 95
 Glu Cys Thr Ala Lys Gly Gly Asn Ala Gly Lys Phe Asp Gly Lys Thr
 100 105 110
 Ile Thr Leu Asn Arg Thr Ala Asp Gly Glu Trp Ser Cys Ala Ser Thr
 115 120 125
 Leu Asp Ala Lys Tyr Lys Pro Gly Lys Cys Ser
 130 135

<210> 141
 <211> 59
 <212> PRT
 <213> Caulobacter crescentus

<400> 141
 Met Thr Lys Phe Val Thr Arg Phe Leu Lys Asp Glu Ser Gly Ala Thr
 1 5 10 15
 Ala Ile Glu Tyr Gly Leu Ile Val Ala Leu Ile Ala Val Val Ile Val
 20 25 30
 Thr Ala Val Thr Thr Leu Gly Thr Asn Leu Arg Thr Ala Phe Thr Lys
 35 40 45
 Ala Gly Ala Ala Val Ser Thr Ala Ala Gly Thr
 50 55

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<210> 142
 <211> 173
 <212> PRT
 <213> Escherichia coli

<400> 142
 Met Ala Val Val Ser Phe Gly Val Asn Ala Ala Pro Thr Ile Pro Gln
 1 5 10 15
 Gly Gln Gly Lys Val Thr Phe Asn Gly Thr Val Val Asp Ala Pro Cys
 20 25 30
 Ser Ile Ser Gln Lys Ser Ala Asp Gln Ser Ile Asp Phe Gly Gln Leu
 35 40 45
 Ser Lys Ser Phe Leu Glu Ala Gly Gly Val Ser Lys Pro Met Asp Leu
 50 55 60
 Asp Ile Glu Leu Val Asn Cys Asp Ile Thr Ala Phe Lys Gly Gly Asn
 65 70 75 80
 Gly Ala Gln Lys Gly Thr Val Lys Leu Ala Phe Thr Gly Pro Ile Val
 85 90 95
 Asn Gly His Ser Asp Glu Leu Asp Thr Asn Gly Gly Thr Gly Thr Ala
 100 105 110
 Ile Val Val Gln Gly Ala Gly Lys Asn Val Val Phe Asp Gly Ser Glu
 115 120 125
 Gly Asp Ala Asn Thr Leu Lys Asp Gly Glu Asn Val Leu His Tyr Thr
 130 135 140
 Ala Val Val Lys Lys Ser Ser Ala Val Gly Ala Ala Val Thr Glu Gly
 145 150 155 160
 Ala Phe Ser Ala Val Ala Asn Phe Asn Leu Thr Tyr Gln
 165 170

<210> 143
 <211> 173
 <212> PRT
 <213> Escherichia coli

<400> 143
 Met Ala Val Val Ser Phe Gly Val Asn Ala Ala Pro Thr Ile Pro Gln
 1 5 10 15
 Gly Gln Gly Lys Val Thr Phe Asn Gly Thr Val Val Asp Ala Pro Cys
 20 25 30
 Ser Ile Ser Gln Lys Ser Ala Asp Gln Ser Ile Asp Phe Gly Gln Leu
 35 40 45
 Ser Lys Ser Phe Leu Glu Ala Gly Gly Val Ser Lys Pro Met Asp Leu
 50 55 60
 Asp Ile Glu Leu Val Asn Cys Asp Ile Thr Ala Phe Lys Gly Gly Asn
 65 70 75 80
 Gly Ala Gln Lys Gly Thr Val Lys Leu Ala Phe Thr Gly Pro Ile Val
 85 90 95

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Asn Gly His Ser Asp Glu Leu Asp Thr Asn Gly Gly Thr Gly Thr Ala
 100 105 110
 Ile Val Val Gln Gly Ala Gly Lys Asn Val Val Phe Asp Gly Ser Glu
 115 120 125
 Gly Asp Ala Asn Thr Leu Lys Asp Gly Glu Asn Val Leu His Tyr Thr
 130 135 140
 Ala Val Val Lys Lys Ser Ser Ala Val Gly Ala Ala Val Thr Glu Gly
 145 150 155 160
 Ala Phe Ser Ala Val Ala Asn Phe Asn Leu Thr Tyr Gln
 165 170

<210> 144
 <211> 172
 <212> PRT
 <213> Escherichia coli

<400> 144
 Met Ala Val Val Ser Phe Gly Val Asn Ala Ala Pro Thr Thr Pro Gln
 1 5 10 15
 Gly Gln Gly Arg Val Thr Phe Asn Gly Thr Val Val Asp Ala Pro Cys
 20 25 30
 Ser Ile Ser Gln Lys Ser Ala Asp Gln Ser Ile Asp Phe Gly Gln Leu
 35 40 45
 Ser Lys Ser Phe Leu Ala Asn Asp Gly Gln Ser Lys Pro Met Asn Leu
 50 55 60
 Asp Ile Glu Leu Val Asn Cys Asp Ile Thr Ala Phe Lys Asn Gly Asn
 65 70 75 80
 Ala Lys Thr Gly Ser Val Lys Leu Ala Phe Thr Gly Pro Thr Val Ser
 85 90 95
 Gly His Pro Ser Glu Leu Ala Thr Asn Gly Gly Pro Gly Thr Ala Ile
 100 105 110
 Met Ile Gln Ala Ala Gly Lys Asn Val Pro Phe Asp Gly Thr Glu Gly
 115 120 125
 Asp Pro Asn Leu Leu Lys Asp Gly Asp Asn Val Leu His Tyr Thr Thr
 130 135 140
 Val Gly Lys Lys Ser Ser Asp Gly Asn Ala Gln Ile Thr Glu Gly Ala
 145 150 155 160
 Phe Ser Gly Val Ala Thr Phe Asn Leu Ser Tyr Gln
 165 170

<210> 145
 <211> 853
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (281) .. (829)

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<400> 145
acgtttctgt ggctcgacgc atcttcctca ttcttctctc caaaaaccac ctcatgcaat 60
ataaacatct ataaataaag ataacaaata gaatattaag ccaacaaata aactgaaaaa 120
gtttgtccgc gatgctttac ctctatgagt caaaatggcc ccaatgtttc atcttttggg 180
ggaaactgtg cagtgttggc agtcaaactc gttgacaaac aaagtgtaca gaacgactgc 240
ccatgtcgat ttagaaatag ttttttgaaa ggaaagcagc atg aaa att aaa act 295
Met Lys Ile Lys Thr
1 5
ctg gca atc gtt gtt ctg tgc gct ctg tcc ctc agt tct acg acg gct 343
Leu Ala Ile Val Val Leu Ser Ala Leu Ser Leu Ser Ser Thr Thr Ala
10 15 20
ctg gcc gct gcc acg acg gtt aat ggt ggg acc gtt cac ttt aaa ggg 391
Leu Ala Ala Ala Thr Thr Val Asn Gly Gly Thr Val His Phe Lys Gly
25 30 35
gaa gtt gtt aac gcc gct tgc gca gtt gat gca ggc tct gtt gat caa 439
Glu Val Val Val Asn Ala Ala Cys Ala Val Asp Ala Gly Ser Val Asp Gln
40 45 50
acc gtt cag tta gga cag gtt cgt acc gca tgc ctg gca cag gaa gga 487
Thr Val Gln Leu Gly Gln Val Arg Thr Ala Ser Leu Ala Gln Glu Gly
55 60 65
gca acc agt tct gct gtc ggt ttt aac att cag ctg aat gat tgc gat 535
Ala Thr Ser Ser Ala Val Gly Phe Asn Ile Gln Leu Asn Asp Cys Asp
70 75 80 85
acc aat gtt gca tct aaa gcc gct gtt gcc ttt tta ggt acg gcg att 583
Thr Asn Val Ala Ser Lys Ala Ala Val Ala Phe Leu Gly Thr Ala Ile
90 95 100
gat gcg ggt cat acc aac gtt ctg gct ctg cag agt tca gct gcg ggt 631
Asp Ala Gly His Thr Asn Val Leu Ala Leu Gln Ser Ser Ala Ala Gly
105 110 115
agc gca aca aac gtt ggt gtg cag atc ctg gac aga acg ggt gct gcg 679
Ser Ala Thr Asn Val Gly Val Gln Ile Leu Asp Arg Thr Gly Ala Ala
120 125 130
ctg acg ctg gat ggt gcg aca ttt agt tca gaa aca acc ctg aat aac 727
Leu Thr Leu Asp Gly Ala Thr Phe Ser Ser Glu Thr Thr Leu Asn Asn
135 140 145
gga acc aat acc att ccg ttc cag gcg cgt tat ttt gca acc ggg gcc 775
Gly Thr Asn Thr Ile Pro Phe Gln Ala Arg Tyr Phe Ala Thr Gly Ala
150 155 160 165
gca acc ccg ggt gct gct aat gcg gat gcg acc ttc aag gtt cag tat 823
Ala Thr Pro Gly Ala Ala Asn Ala Asp Ala Thr Phe Lys Val Gln Tyr
170 175 180
caa taa cctacctagg ttcagggacg ttca 853
Gln

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<210> 146

<211> 182

<212> PRT

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<213> Escherichia coli

<400> 146

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Met Lys Ile Lys Thr Leu Ala Ile Val Val Leu Ser Ala Leu Ser Leu
 1          5          10          15
Ser Ser Thr Thr Ala Leu Ala Ala Ala Thr Thr Val Asn Gly Gly Thr
          20          25          30
Val His Phe Lys Gly Glu Val Val Asn Ala Ala Cys Ala Val Asp Ala
          35          40          45
Gly Ser Val Asp Gln Thr Val Gln Leu Gly Gln Val Arg Thr Ala Ser
          50          55          60
Leu Ala Gln Glu Gly Ala Thr Ser Ser Ala Val Gly Phe Asn Ile Gln
          65          70          75          80
Leu Asn Asp Cys Asp Thr Asn Val Ala Ser Lys Ala Ala Val Ala Phe
          85          90          95
Leu Gly Thr Ala Ile Asp Ala Gly His Thr Asn Val Leu Ala Leu Gln
          100          105          110
Ser Ser Ala Ala Gly Ser Ala Thr Asn Val Gly Val Gln Ile Leu Asp
          115          120          125
Arg Thr Gly Ala Ala Leu Thr Leu Asp Gly Ala Thr Phe Ser Ser Glu
          130          135          140
Thr Thr Leu Asn Asn Gly Thr Asn Thr Ile Pro Phe Gln Ala Arg Tyr
          145          150          155          160
Phe Ala Thr Gly Ala Ala Thr Pro Gly Ala Ala Asn Ala Asp Ala Thr
          165          170          175
Phe Lys Val Gln Tyr Gln
          180

```

<210> 147

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: FLAG peptide

<400> 147

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Cys Gly Gly Asp Tyr Lys Asp Asp Asp Asp Lys
 1          5          10

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<210> 148

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 148

ccggaattca tggacattga cccttataaa g

31

<210> 149

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

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<400> 149
gtgcagtatg gtgaggtgag gaatgctcag gagactc 37

<210> 150
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 150
gsgtctcctg agcattcctc acctcaccat actgcac 37

<210> 151
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 151
cttccaaaag tgagggaaga aatgtgaaac cac 33

<210> 152
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 152
cgcggtcccaa gcttctaaac aacagtagtc tccggaagcg ttgatag 47

<210> 153
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 153
gtgggtttcac atttcttccc tcacttttgg aag 33

<210> 154
<211> 281
<212> PRT
<213> Saccharomyces cerevisiae

<400> 154
Met Ser Glu Tyr Gln Pro Ser Leu Phe Ala Leu Asn Pro Met Gly Phe
1 5 10 15

Ser Pro Leu Asp Gly Ser Lys Ser Thr Asn Glu Asn Val Ser Ala Ser
20 25 30

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Thr Ser Thr Ala Lys Pro Met Val Gly Gln Leu Ile Phe Asp Lys Phe
      35              40              45

Ile Lys Thr Glu Glu Asp Pro Ile Ile Lys Gln Asp Thr Pro Ser Asn
      50              55              60

Leu Asp Phe Asp Phe Ala Leu Pro Gln Thr Ala Thr Ala Pro Asp Ala
      65              70              75              80

Lys Thr Val Leu      Pro Ile Pro Glu Leu Asp Asp Ala Val Val Glu Ser
              85              90              95
Phe Phe Ser Ser Ser Thr Asp Ser Thr Pro Met Phe Glu Tyr Glu Asn
              100              105              110

Leu Glu Asp Asn Ser Lys Glu Trp Thr Ser Leu Phe Asp Asn Asp Ile
      115              120              125

Pro Val Thr Thr Asp Asp Val Ser Leu Ala Asp Lys Ala Ile Glu Ser
      130              135              140

Thr Glu Glu Val Ser      Leu Val Pro Ser Asn Leu Glu Val Ser Thr Thr
      145              150              155              160

Ser Phe Leu Pro Thr Pro Val Leu Glu Asp Ala Lys Leu Thr Gln Thr
              165              170              175

Arg Lys Val Lys Lys Pro Asn Ser Val Val Lys Lys Ser His His Val
              180              185              190

Gly Lys Asp Asp Glu Ser Arg Leu Asp His Leu Gly Val Val Ala Tyr
      195              200              205

Asn Arg Lys Gln Arg Ser Ile Pro Leu Ser Pro Ile Val Pro Glu Ser
      210              215              220

Ser Asp Pro Ala Ala Leu Lys Arg Ala Arg Asn Thr Glu Ala Ala Arg
      225              230              235              240

Arg Ser Arg Ala Arg Lys Leu Gln Arg Met Lys Gln Leu Glu Asp Lys
              245              250              255

Val Glu Glu Leu Leu Ser Lys Asn Tyr His Leu Glu Asn Glu Val Ala
      260              265              270

Arg Leu Lys Lys Leu Val Gly Glu Arg
      275              280

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<210> 155

<211> 181

<212> PRT

<213> Escherichia coli

<400> 155

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Met Lys Ile Lys Thr Leu Ala Ile Val Val Leu Ser Ala Leu Ser Leu
  1              5              10              15

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```

Ser Ser Thr Ala Ala Leu Ala Ala Ala Thr Thr Val Asn Gly Gly Thr
      20              25              30

```

```

Val His Phe Lys Gly Glu Val Val Asn Ala Ala Cys Ala Val Asp Ala
      35              40              45

```

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Gly Ser Val Asp Gln Thr Val Gln Leu Gly Gln Val Arg Thr Ala Ser
50 55 60

Leu Ala Gln Glu Gly Ala Thr Ser Ser Ala Val Gly Phe Asn Ile Gln
65 70 75 80

Leu Asn Asp Cys Asp Thr Asn Val Ala Ser Lys Ala Ala Val Ala Phe
85 90 95

Leu Gly Thr Ala Ile Asp Ala Gly His Thr Asn Val Leu Ala Leu Gln
100 105 110

Ser Ser Ala Ala Gly Ser Ala Thr Asn Val Gly Val Gln Ile Leu Asp
115 120 125

Arg Thr Gly Ala Ala Leu Thr Leu Asp Gly Ala Thr Phe Ser Ser Glu
130 135 140

Thr Thr Leu Asn Asn Gly Thr Asn Thr Ile Pro Phe Gln Ala Arg Tyr
145 150 155 160

Phe Ala Gly Ala Ala Thr Pro Gly Ala Ala Asn Ala Asp Ala Thr Phe
165 170 175

Lys Val Gln Tyr Gln
180

<210> 156
<211> 447
<212> DNA
<213> Hepatitis B

<220>
<221> CDS
<222> (1)..(447)

<400> 156
atg gac att gac cct tat aaa gaa ttt gga gct act gtg gag tta ctc 48
Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
1 5 10 15

tgc ttt ttg cct tct gac ttc ttt cct tcc gta cga gat ctt cta gat 96
Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
20 25 30

acc gcc gca gct ctg tat cgg gat gcc tta gag tct cct gag cat tgt 144
Thr Ala Ala Ala Leu Tyr Arg Asp Ala Leu Glu Ser Pro Glu His Cys
35 40 45

tca cct cac cat act gca ctc agg caa gca att ctt tgc tgg gga gac 192
Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Asp
50 55 60

tta atg act cta gct acc tgg gtg ggt act aat tta gaa gat cca gca 240
Leu Met Thr Leu Ala Thr Trp Val Gly Thr Asn Leu Glu Asp Pro Ala
65 70 75 80

tct agg gac cta gta gtc agt tat gtc aac act aat gtg ggc cta aag 288
Ser Arg Asp Leu Val Ser Tyr Val Asn Thr Asn Val Gly Leu Lys
85 90 95

ttc aga caa tta ttg tgg ttt cac att tct tgt ctc act ttt gga aga 336
Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg

208T0-2080500T

100	105	110	
gaa acg gtt cta gag tat ttg gtc tct ttt gga gtg tgg att cgc act			384
Glu Thr Val Leu Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr			
115	120	125	
cct cca gcc tat aga cca cca aat gcc cct atc cta tca acg ctt ccg			432
Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro			
130	135	140	
gag act act gtt gtt			447
Glu Thr Thr Val Val			
145			

<210> 157
 <211> 149
 <212> PRT
 <213> Hepatitis B

<400> 157
 Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
 1 5 10 15
 Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
 20 25 30
 Thr Ala Ala Ala Leu Tyr Arg Asp Ala Leu Glu Ser Pro Glu His Cys
 35 40 45
 Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Asp
 50 55 60
 Leu Met Thr Leu Ala Thr Trp Val Gly Thr Asn Leu Glu Asp Pro Ala
 65 70 75 80
 Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Val Gly Leu Lys
 85 90 95
 Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
 100 105 110
 Glu Thr Val Leu Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
 115 120 125
 Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
 130 135 140
 Glu Thr Thr Val Val
 145

<210> 158
 <211> 152
 <212> PRT
 <213> Hepatitis B

<400> 158
 Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
 1 5 10 15
 Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp

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<213> Bacteriophage R 17

<400> 160

Ala Ser Asn Phe Thr Gln Phe Val Leu Val Asn Asp Gly Gly Thr Gly
1 5 10 15
Asn Val Thr Val Ala Pro Ser Asn Phe Ala Asn Gly Val Ala Glu Trp
20 25 30
Ile Ser Ser Asn Ser Arg Ser Gln Ala Tyr Lys Val Thr Cys Ser Val
35 40 45
Arg Gln Ser Ser Ala Gln Asn Arg Lys Tyr Thr Ile Lys Val Glu Val
50 55 60
Pro Lys Val Ala Thr Gln Thr Val Gly Gly Val Glu Leu Pro Val Ala
65 70 75 80
Ala Trp Arg Ser Tyr Leu Asn Met Glu Leu Thr Ile Pro Ile Phe Ala
85 90 95
Thr Asn Ser Asp Cys Glu Leu Ile Val Lys Ala Met Gln Gly Leu Leu
100 105 110
Lys Asp Gly Asn Pro Ile Pro Ser Ala Ile Ala Ala Asn Ser Gly Ile
115 120 125

Tyr

<210> 161

<211> 130

<212> PRT

<213> Bacteriophage fr

<400> 161

Met Ala Ser Asn Phe Glu Glu Phe Val Leu Val Asp Asn Gly Gly Thr
1 5 10 15
Gly Asp Val Lys Val Ala Pro Ser Asn Phe Ala Asn Gly Val Ala Glu
20 25 30
Trp Ile Ser Ser Asn Ser Arg Ser Gln Ala Tyr Lys Val Thr Cys Ser
35 40 45
Val Arg Gln Ser Ser Ala Asn Asn Arg Lys Tyr Thr Val Lys Val Glu
50 55 60
Val Pro Lys Val Ala Thr Gln Val Gln Gly Gly Val Glu Leu Pro Val
65 70 75 80
Ala Ala Trp Arg Ser Tyr Met Asn Met Glu Leu Thr Ile Pro Val Phe
85 90 95
Ala Thr Asn Asp Asp Cys Ala Leu Ile Val Lys Ala Leu Gln Gly Thr
100 105 110
Phe Lys Thr Gly Asn Pro Ile Ala Thr Ala Ile Ala Ala Asn Ser Gly
115 120 125

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Ile Tyr
130

<210> 162
<211> 130
<212> PRT
<213> Bacteriophage GA

<400> 162

Met Ala Thr Leu Arg Ser Phe Val Leu Val Asp Asn Gly Gly Thr Gly
1 5 10 15
Asn Val Thr Val Val Pro Val Ser Asn Ala Asn Gly Val Ala Glu Trp
20 25 30
Leu Ser Asn Asn Ser Arg Ser Gln Ala Tyr Arg Val Thr Ala Ser Tyr
35 40 45
Arg Ala Ser Gly Ala Asp Lys Arg Lys Tyr Ala Ile Lys Leu Glu Val
50 55 60
Pro Lys Ile Val Thr Gln Val Val Asn Gly Val Glu Leu Pro Gly Ser
65 70 75 80
Ala Trp Lys Ala Tyr Ala Ser Ile Asp Leu Thr Ile Pro Ile Phe Ala
85 90 95
Ala Thr Asp Asp Val Thr Val Ile Ser Lys Ser Leu Ala Gly Leu Phe
100 105 110
Lys Val Gly Asn Pro Ile Ala Glu Ala Ile Ser Ser Gln Ser Gly Phe
115 120 125
Tyr Ala
130

<210> 163
<211> 132
<212> PRT
<213> Bacteriophage SP

<400> 163

Met Ala Lys Leu Asn Gln Val Thr Leu Ser Lys Ile Gly Lys Asn Gly
1 5 10 15
Asp Gln Thr Leu Thr Leu Thr Pro Arg Gly Val Asn Pro Thr Asn Gly
20 25 30
Val Ala Ser Leu Ser Glu Ala Gly Ala Val Pro Ala Leu Glu Lys Arg
35 40 45
Val Thr Val Ser Val Ala Gln Pro Ser Arg Asn Arg Lys Asn Phe Lys
50 55 60
Val Gln Ile Lys Leu Gln Asn Pro Thr Ala Cys Thr Arg Asp Ala Cys
65 70 75 80

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Asp Pro Ser Val Thr Arg Ser Ala Phe Ala Asp Val Thr Leu Ser Phe
85 90 95
Thr Ser Tyr Ser Thr Asp Glu Glu Arg Ala Leu Ile Arg Thr Glu Leu
100 105 110
Ala Ala Leu Leu Ala Asp Pro Leu Ile Val Asp Ala Ile Asp Asn Leu
115 120 125
Asn Pro Ala Tyr
130

<210> 164
<211> 130
<212> PRT
<213> Bacteriophage MS2

<400> 164

Met Ala Ser Asn Phe Thr Gln Phe Val Leu Val Asp Asn Gly Gly Thr
1 5 10 15
Gly Asp Val Thr Val Ala Pro Ser Asn Phe Ala Asn Gly Val Ala Glu
20 25 30
Trp Ile Ser Ser Asn Ser Arg Ser Gln Ala Tyr Lys Val Thr Cys Ser
35 40 45
Val Arg Gln Ser Ser Ala Gln Asn Arg Lys Tyr Thr Ile Lys Val Glu
50 55 60
Val Pro Lys Val Ala Thr Gln Thr Val Gly Gly Val Glu Leu Pro Val
65 70 75 80
Ala Ala Trp Arg Ser Tyr Leu Asn Met Glu Leu Thr Ile Pro Ile Phe
85 90 95
Ala Thr Asn Ser Asp Cys Glu Leu Ile Val Lys Ala Met Gln Gly Leu
100 105 110
Leu Lys Asp Gly Asn Pro Ile Pro Ser Ala Ile Ala Ala Asn Ser Gly
115 120 125
Ile Tyr
130

<210> 165
<211> 133
<212> PRT
<213> Bacteriophage M11

<400> 165

Met Ala Lys Leu Gln Ala Ile Thr Leu Ser Gly Ile Gly Lys Lys Gly
1 5 10 15
Asp Val Thr Leu Asp Leu Asn Pro Arg Gly Val Asn Pro Thr Asn Gly
20 25 30
Val Ala Ala Leu Ser Glu Ala Gly Ala Val Pro Ala Leu Glu Lys Arg
35 40 45

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Val Thr Ile Ser Val Ser Gln Pro Ser Arg Asn Arg Lys Asn Tyr Lys
50 55 60

Val Gln Val Lys Ile Gln Asn Pro Thr Ser Cys Thr Ala Ser Gly Thr
65 70 75 80

Cys Asp Pro Ser Val Thr Arg Ser Ala Tyr Ser Asp Val Thr Phe Ser
85 90 95

Phe Thr Gln Tyr Ser Thr Val Glu Glu Arg Ala Leu Val Arg Thr Glu
100 105 110

Leu Gln Ala Leu Leu Ala Asp Pro Met Leu Val Asn Ala Ile Asp Asn
115 120 125

Leu Asn Pro Ala Tyr
130

<210> 166
<211> 133
<212> PRT
<213> Bacteriophage MX1

<400> 166
Met Ala Lys Leu Gln Ala Ile Thr Leu Ser Gly Ile Gly Lys Asn Gly
1 5 10 15

Asp Val Thr Leu Asn Leu Asn Pro Arg Gly Val Asn Pro Thr Asn Gly
20 25 30

Val Ala Ala Leu Ser Glu Ala Gly Ala Val Pro Ala Leu Glu Lys Arg
35 40 45

Val Thr Ile Ser Val Ser Gln Pro Ser Arg Asn Arg Lys Asn Tyr Lys
50 55 60

Val Gln Val Lys Ile Gln Asn Pro Thr Ser Cys Thr Ala Ser Gly Thr
65 70 75 80

Cys Asp Pro Ser Val Thr Arg Ser Ala Tyr Ala Asp Val Thr Phe Ser
85 90 95

Phe Thr Gln Tyr Ser Thr Asp Glu Glu Arg Ala Leu Val Arg Thr Glu
100 105 110

Leu Lys Ala Leu Leu Ala Asp Pro Met Leu Ile Asp Ala Ile Asp Asn
115 120 125

Leu Asn Pro Ala Tyr
130

<210> 167
<211> 330
<212> PRT
<213> Bacteriophage NL95

<400> 167
Met Ala Lys Leu Asn Lys Val Thr Leu Thr Gly Ile Gly Lys Ala Gly
1 5 10 15

Asn Gln Thr Leu Thr Leu Thr Pro Arg Gly Val Asn Pro Thr Asn Gly

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20					25					30					
Val	Ala	Ser	Leu	Ser	Glu	Ala	Gly	Ala	Val	Pro	Ala	Leu	Glu	Lys	Arg
		35					40					45			
Val	Thr	Val	Ser	Val	Ala	Gln	Pro	Ser	Arg	Asn	Arg	Lys	Asn	Tyr	Lys
	50					55					60				
Val	Gln	Ile	Lys	Leu	Gln	Asn	Pro	Thr	Ala	Cys	Thr	Lys	Asp	Ala	Cys
65					70					75					80
Asp	Pro	Ser	Val	Thr	Arg	Ser	Gly	Ser	Arg	Asp	Val	Thr	Leu	Ser	Phe
				85					90					95	
Thr	Ser	Tyr	Ser	Thr	Glu	Arg	Glu	Arg	Ala	Leu	Ile	Arg	Thr	Glu	Leu
			100					105					110		
Ala	Ala	Leu	Leu	Lys	Asp	Asp	Leu	Ile	Val	Asp	Ala	Ile	Asp	Asn	Leu
		115					120					125			
Asn	Pro	Ala	Tyr	Trp	Ala	Ala	Leu	Leu	Ala	Ala	Ser	Pro	Gly	Gly	Gly
	130					135					140				
Asn	Asn	Pro	Tyr	Pro	Gly	Val	Pro	Asp	Ser	Pro	Asn	Val	Lys	Pro	Pro
145					150					155					160
Gly	Gly	Thr	Gly	Thr	Tyr	Arg	Cys	Pro	Phe	Ala	Cys	Tyr	Arg	Arg	Gly
				165					170					175	
Glu	Leu	Ile	Thr	Glu	Ala	Lys	Asp	Gly	Ala	Cys	Ala	Leu	Tyr	Ala	Cys
			180					185					190		
Gly	Ser	Glu	Ala	Leu	Val	Glu	Phe	Glu	Tyr	Ala	Leu	Glu	Asp	Phe	Leu
		195					200					205			
Gly	Asn	Glu	Phe	Trp	Arg	Asn	Trp	Asp	Gly	Arg	Leu	Ser	Lys	Tyr	Asp
	210					215					220				
Ile	Glu	Thr	His	Arg	Arg	Cys	Arg	Gly	Asn	Gly	Tyr	Val	Asp	Leu	Asp
225					230					235					240
Ala	Ser	Val	Met	Gln	Ser	Asp	Glu	Tyr	Val	Leu	Ser	Gly	Ala	Tyr	Asp
				245					250					255	
Val	Val	Lys	Met	Gln	Pro	Pro	Gly	Thr	Phe	Asp	Ser	Pro	Arg	Tyr	Tyr
			260					265					270		
Leu	His	Leu	Met	Asp	Gly	Ile	Tyr	Val	Asp	Leu	Ala	Glu	Val	Thr	Ala
		275					280					285			
Tyr	Arg	Ser	Tyr	Gly	Met	Val	Ile	Gly	Phe	Trp	Thr	Asp	Ser	Lys	Ser
	290					295					300				
Pro	Gln	Leu	Pro	Thr	Asp	Phe	Thr	Arg	Phe	Asn	Arg	His	Asn	Cys	Pro
305					310					315					320
Val	Gln	Thr	Val	Ile	Val	Ile	Pro	Ser	Leu						
				325					330						

<210> 168
 <211> 134
 <212> PRT

208110-20605001

<213> Apis mellifera

<400> 168

Ile Ile Tyr Pro Gly Thr Leu Trp Cys Gly His Gly Asn Lys Ser Ser
1 5 10 15
Gly Pro Asn Glu Leu Gly Arg Phe Lys His Thr Asp Ala Cys Cys Arg
20 25 30
Thr His Asp Met Cys Pro Asp Val Met Ser Ala Gly Glu Ser Lys His
35 40 45
Gly Leu Thr Asn Thr Ala Ser His Thr Arg Leu Ser Cys Asp Cys Asp
50 55 60
Asp Lys Phe Tyr Asp Cys Leu Lys Asn Ser Ala Asp Thr Ile Ser Ser
65 70 75 80
Tyr Phe Val Gly Lys Met Tyr Phe Asn Leu Ile Asp Thr Lys Cys Tyr
85 90 95
Lys Leu Glu His Pro Val Thr Gly Cys Gly Glu Arg Thr Glu Gly Arg
100 105 110
Cys Leu His Tyr Thr Val Asp Lys Ser Lys Pro Lys Val Tyr Gln Trp
115 120 125
Phe Asp Leu Arg Lys Tyr
130

<210> 169

<211> 129

<212> PRT

<213> Apis mellifera

<400> 169

Ile Ile Tyr Pro Gly Thr Leu Trp Cys Gly His Gly Asn Lys Ser Ser
1 5 10 15
Gly Pro Asn Glu Leu Gly Arg Phe Lys His Thr Asp Ala Cys Cys Arg
20 25 30
Thr His Asp Met Cys Pro Asn Val Met Ser Ala Gly Glu Ser Lys His
35 40 45
Gly Leu Thr Asp Thr Ala Ser Arg Leu Ser Cys Asn Asp Asn Asp Leu
50 55 60
Phe Tyr Lys Asp Ser Ala Asp Thr Ile Ser Ser Tyr Phe Val Gly Lys
65 70 75 80
Met Tyr Phe Asn Leu Ile Asn Thr Lys Cys Tyr Lys Leu Glu His Pro
85 90 95
Val Thr Gly Cys Gly Glu Arg Thr Glu Gly Arg Cys Leu His Tyr Thr
100 105 110
Val Asp Lys Ser Lys Pro Lys Val Tyr Gln Trp Phe Asp Leu Arg Lys
115 120 125
Tyr

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<210> 170
 <211> 134
 <212> PRT
 <213> Apis dorsata

<400> 170
 Ile Ile Tyr Pro Gly Thr Leu Trp Cys Gly His Gly Asn Val Ser Ser
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 Ser Pro Asp Glu Leu Gly Arg Phe Lys His Thr Asp Ser Cys Cys Arg
 20 25 30
 Ser His Asp Met Cys Pro Asp Val Met Ser Ala Gly Glu Ser Lys His
 35 40 45
 Gly Leu Thr Asn Thr Ala Ser His Thr Arg Leu Ser Cys Asp Cys Asp
 50 55 60
 Asp Lys Phe Tyr Asp Cys Leu Lys Asn Ser Ser Asp Thr Ile Ser Ser
 65 70 75 80
 Tyr Phe Val Gly Glu Met Tyr Phe Asn Ile Leu Asp Thr Lys Cys Tyr
 85 90 95
 Lys Leu Glu His Pro Val Thr Gly Cys Gly Lys Arg Thr Glu Gly Arg
 100 105 110
 Cys Leu Asn Tyr Thr Val Asp Lys Ser Lys Pro Lys Val Tyr Gln Trp
 115 120 125
 Phe Asp Leu Arg Lys Tyr
 130

<210> 171
 <211> 134
 <212> PRT
 <213> Apis cerana

<400> 171
 Ile Ile Tyr Pro Gly Thr Leu Trp Cys Gly His Gly Asn Val Ser Ser
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 Gly Pro Asn Glu Leu Gly Arg Phe Lys His Thr Asp Ala Cys Cys Arg
 20 25 30
 Thr His Asp Met Cys Pro Asp Val Met Ser Ala Gly Glu Ser Lys His
 35 40 45
 Gly Leu Thr Asn Thr Ala Ser His Thr Arg Leu Ser Cys Asp Cys Asp
 50 55 60
 Asp Thr Phe Tyr Asp Cys Leu Lys Asn Ser Gly Glu Lys Ile Ser Ser
 65 70 75 80
 Tyr Phe Val Gly Lys Met Tyr Phe Asn Leu Ile Asp Thr Lys Cys Tyr
 85 90 95
 Lys Leu Glu His Pro Val Thr Gly Cys Gly Glu Arg Thr Glu Gly Arg
 100 105 110
 Cys Leu Arg Tyr Thr Val Asp Lys Ser Lys Pro Lys Val Tyr Gln Trp
 115 120 125

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Phe Asp Leu Arg Lys Tyr
130

<210> 172
<211> 136
<212> PRT
<213> Bombus pennsylvanicus

<400> 172

Ile	Ile	Tyr	Pro	Gly	Thr	Leu	Trp	Cys	Gly	Asn	Gly	Asn	Ile	Ala	Asn	
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		20						25					30			
Thr	His	Asp	Met	Cys	Pro	Asp	Ile	Ile	Glu	Ala	His	Gly	Ser	Lys	His	
		35					40					45				
Gly	Leu	Thr	Asn	Pro	Ala	Asp	Tyr	Thr	Arg	Leu	Asn	Cys	Glu	Cys	Asp	
	50					55					60					
Glu	Glu	Phe	Arg	His	Cys	Leu	His	Asn	Ser	Gly	Asp	Ala	Val	Ser	Ala	
65				70						75					80	
Ala	Phe	Val	Gly	Arg	Thr	Tyr	Phe	Thr	Ile	Leu	Gly	Thr	Gln	Cys	Phe	
				85					90					95		
Arg	Leu	Asp	Tyr	Pro	Ile	Val	Lys	Cys	Lys	Val	Lys	Ser	Thr	Ile	Leu	
			100					105					110			
Arg	Glu	Cys	Lys	Glu	Tyr	Glu	Phe	Asp	Thr	Asn	Ala	Pro	Gln	Lys	Tyr	
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Gln	Trp	Phe	Asp	Val	Leu	Ser	Tyr									
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<211> 142
<212> PRT
<213> Heloderma suspectum

<400> 173

Gly	Ala	Phe	Ile	Met	Pro	Gly	Thr	Leu	Trp	Cys	Gly	Ala	Gly	Asn	Ala	
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		20						25					30			
Cys	Arg	Asp	His	Asp	His	Cys	Ser	Asp	Thr	Met	Ala	Ala	Leu	Glu	Tyr	
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Lys	His	Gly	Met	Arg	Asn	Tyr	Arg	Pro	His	Thr	Val	Ser	His	Cys	Asp	
	50					55					60					
Cys	Asp	Asn	Gln	Phe	Arg	Ser	Cys	Leu	Met	Asn	Val	Lys	Asp	Arg	Thr	
65				70						75				80		
Ala	Asp	Leu	Val	Gly	Met	Thr	Tyr	Phe	Thr	Val	Leu	Lys	Ile	Ser	Cys	
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Phe Glu Leu Glu Glu Gly Glu Gly Cys Val Asp Asn Asn Phe Ser Gln
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 Gln Cys Thr Lys Ser Glu Ile Met Pro Val Ala Lys Leu Val Ser Ala
 115 120 125
 Ala Pro Tyr Gln Ala Gln Ala Glu Thr Gln Ser Gly Glu Gly
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<210> 174
 <211> 143
 <212> PRT
 <213> Heloderma suspectum

<400> 174
 Gly Ala Phe Ile Met Pro Gly Thr Leu Trp Cys Gly Ala Gly Asn Ala
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 Ala Ser Asp Tyr Ser Gln Leu Gly Thr Glu Lys Asp Thr Asp Met Cys
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 Cys Arg Asp His Asp His Cys Glu Asn Trp Ile Ser Ala Leu Glu Tyr
 35 40 45
 Lys His Gly Met Arg Asn Tyr Tyr Pro Ser Thr Ile Ser His Cys Asp
 50 55 60
 Cys Asp Asn Gln Phe Arg Ser Cys Leu Met Lys Leu Lys Asp Gly Thr
 65 70 75 80
 Ala Asp Tyr Val Gly Gln Thr Tyr Phe Asn Val Leu Lys Ile Pro Cys
 85 90 95
 Phe Glu Leu Glu Glu Gly Glu Gly Cys Val Asp Trp Asn Phe Trp Leu
 100 105 110
 Glu Cys Thr Glu Ser Lys Ile Met Pro Val Ala Lys Leu Val Ser Ala
 115 120 125
 Ala Pro Tyr Gln Ala Gln Ala Glu Thr Gln Ser Gly Glu Gly Arg
 130 135 140

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 <211> 142
 <212> PRT
 <213> Heloderma suspectum

<400> 175
 Gly Ala Phe Ile Met Pro Gly Thr Leu Trp Cys Gly Ala Gly Asn Ala
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 Ala Ser Asp Tyr Ser Gln Leu Gly Thr Glu Lys Asp Thr Asp Met Cys
 20 25 30
 Cys Arg Asp His Asp His Cys Glu Asn Trp Ile Ser Ala Leu Glu Tyr
 35 40 45
 Lys His Gly Met Arg Asn Tyr Tyr Pro Ser Thr Ile Ser His Cys Asp
 50 55 60
 Cys Asp Asn Gln Phe Arg Ser Cys Leu Met Lys Leu Lys Asp Gly Thr

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65					70						75				80
Ala	Asp	Tyr	Val	Gly	Gln	Thr	Tyr	Phe	Asn	Val	Leu	Lys	Ile	Pro	Cys
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Phe	Glu	Leu	Glu	Glu	Gly	Glu	Gly	Cys	Val	Asp	Trp	Asn	Phe	Trp	Leu
			100					105					110		
Glu	Cys	Thr	Glu	Ser	Lys	Ile	Met	Pro	Val	Ala	Lys	Leu	Val	Ser	Ala
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 <212> PRT
 <213> IgE heavy chain

<400> 176

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Gly	Ala	Ser	Val	Arg	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Ile
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Asp	Ser	Tyr	Ile	His	Trp	Ile	Arg	Gln	Ala	Pro	Gly	His	Gly	Leu	Glu
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Trp	Val	Gly	Trp	Ile	Asn	Pro	Asn	Ser	Gly	Gly	Thr	Asn	Tyr	Ala	Pro
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Arg	Phe	Gln	Gly	Arg	Val	Thr	Met	Thr	Arg	Asp	Ala	Ser	Phe	Ser	Thr
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Ala	Tyr	Met	Asp	Leu	Arg	Ser	Leu	Arg	Ser	Asp	Asp	Ser	Ala	Val	Phe
			100					105					110		
Tyr	Cys	Ala	Lys	Ser	Asp	Pro	Phe	Trp	Ser	Asp	Tyr	Tyr	Asn	Phe	Asp
		115					120					125			
Tyr	Ser	Tyr	Thr	Leu	Asp	Val	Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr	Val
	130					135					140				
Ser	Ser	Ala	Ser	Thr	Gln	Ser	Pro	Ser	Val	Phe	Pro	Leu	Thr	Arg	Cys
145					150					155					160
Cys	Lys	Asn	Ile	Pro	Ser	Asn	Ala	Thr	Ser	Val	Thr	Leu	Gly	Cys	Leu
				165					170					175	
Ala	Thr	Gly	Tyr	Phe	Pro	Glu	Pro	Val	Met	Val	Thr	Trp	Asp	Thr	Gly
			180					185					190		
Ser	Leu	Asn	Gly	Thr	Thr	Met	Thr	Leu	Pro	Ala	Thr	Thr	Leu	Thr	Leu
		195					200					205			
Ser	Gly	His	Tyr	Ala	Thr	Ile	Ser	Leu	Leu	Thr	Val	Ser	Gly	Ala	Trp
	210					215					220				

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Ala	Lys	Gln	Met	Phe	Thr	Cys	Arg	Val	Ala	His	Thr	Pro	Ser	Ser	Thr
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Pro	Pro	Thr	Val	Lys	Ile	Leu	Gln	Ser	Ser	Cys	Asp	Gly	Gly	Gly	His
			260					265					270		
Phe	Pro	Pro	Thr	Ile	Gln	Leu	Leu	Cys	Leu	Val	Ser	Gly	Tyr	Thr	Pro
		275					280					285			
Gly	Thr	Ile	Asn	Ile	Thr	Trp	Leu	Glu	Asp	Gly	Gln	Val	Met	Asp	Val
	290					295					300				
Asp	Leu	Ser	Thr	Ala	Ser	Thr	Thr	Gln	Glu	Gly	Glu	Leu	Ala	Ser	Thr
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Gln	Ser	Glu	Leu	Thr	Leu	Ser	Gln	Lys	His	Trp	Leu	Ser	Asp	Arg	Thr
				325					330					335	
Tyr	Thr	Cys	Gln	Val	Thr	Tyr	Gln	Gly	His	Thr	Phe	Glu	Asp	Ser	Thr
			340					345					350		
Lys	Lys	Cys	Ala	Asp	Ser	Asn	Pro	Arg	Gly	Val	Ser	Ala	Tyr	Leu	Ser
		355					360					365			
Arg	Pro	Ser	Pro	Phe	Asp	Leu	Phe	Ile	Arg	Lys	Ser	Pro	Thr	Ile	Thr
	370					375					380				
Cys	Leu	Val	Val	Asp	Leu	Ala	Pro	Ser	Lys	Gly	Thr	Val	Asn	Leu	Thr
385					390					395					400
Trp	Ser	Arg	Ala	Ser	Gly	Lys	Pro	Val	Asn	His	Ser	Thr	Arg	Lys	Glu
				405					410					415	
Glu	Lys	Gln	Arg	Asn	Gly	Thr	Leu	Thr	Val	Thr	Ser	Thr	Leu	Pro	Val
			420					425					430		
Gly	Thr	Arg	Asp	Trp	Ile	Glu	Gly	Glu	Thr	Tyr	Gln	Cys	Arg	Val	Thr
		435					440					445			
His	Pro	His	Leu	Pro	Arg	Ala	Leu	Met	Arg	Ser	Thr	Thr	Lys	Thr	Ser
	450					455					460				
Gly	Pro	Arg	Ala	Ala	Pro	Glu	Val	Tyr	Ala	Phe	Ala	Thr	Pro	Glu	Trp
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Pro	Gly	Ser	Arg	Asp	Lys	Arg	Thr	Leu	Ala	Cys	Leu	Ile	Gln	Asn	Phe
				485					490					495	
Met	Pro	Glu	Asp	Ile	Ser	Val	Gln	Trp	Leu	His	Asn	Glu	Val	Gln	Leu
			500					505					510		
Pro	Asp	Ala	Arg	His	Ser	Thr	Thr	Gln	Pro	Arg	Lys	Thr	Lys	Gly	Ser
		515					520					525			
Gly	Phe	Phe	Val	Phe	Ser	Arg	Leu	Glu	Val	Thr	Arg	Ala	Glu	Trp	Glu
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Gln	Lys	Asp	Glu	Phe	Ile	Cys	Arg	Ala	Val	His	Glu	Ala	Ala	Ser	Pro
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Ser Gln Thr Val Gln Arg Ala Val Ser Val Asn Pro Gly Lys
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Cys Gly Gly Val Asn Leu Thr Trp Ser Arg Ala Ser Gly
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<400> 179
Ile Asn His Arg Gly Tyr Trp Val
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<210> 180
<211> 8
<212> PRT
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<400> 180
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<210> 182
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<210> 183
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<400> 183
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<210> 188
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<210> 189
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<212> PRT
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<400> 189
Gly Thr Val Ser Thr Leu Ser
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<400> 195
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<212> DNA
<213> Oligonucleotide Primer

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<210> 198
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8464

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<212> PRT
<213> Ce3epitope

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1 5 10

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<400> 208
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1 5 10

<210> 209
<211> 9
<212> PRT
<213> Bee venom phospholipase A2 cloning vector

<400> 209
Ala Ala Ala Ser Gly Gly Cys Gly Gly
1 5

<210> 210
<211> 145
<212> PRT
<213> PLA₂ fusion protein

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Ser Ser Gly Pro Asn Glu Leu Gly Arg Phe Lys His Thr Asp Ala Cys
20 25 30

Cys Arg Thr Gln Asp Met Cys Pro Asp Val Met Ser Ala Gly Glu Ser
35 40 45

Lys His Gly Leu Thr Asn Thr Ala Ser His Thr Arg Leu Ser Cys Asp
50 55 60

Cys Asp Asp Lys Phe Tyr Asp Cys Leu Lys Asn Ser Ala Asp Thr Ile
65 70 75 80

Ser Ser Tyr Phe Val Gly Lys Met Tyr Phe Asn Leu Ile Asp Thr Lys
85 90 95

Cys Tyr Lys Leu Glu His Pro Val Thr Gly Cys Gly Glu Arg Thr Glu
100 105 110

Gly Arg Cys Leu His Tyr Thr Val Asp Lys Ser Lys Pro Lys Val Tyr
115 120 125

Gln Trp Phe Asp Leu Arg Lys Tyr Ala Ala Ala Ser Gly Gly Cys Gly
130 135 140

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Gly
145

<210> 211
<211> 17
<212> PRT
<213> Ce4mimotope

<400> 211
Gly Glu Phe Cys Ile Asn His Arg Gly Tyr Trp Val Cys Gly Asp Pro
1 5 10 15

Ala

<210> 212
<211> 27
<212> PRT
<213> Synthetic M2 Peptide

<400> 212
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Arg Cys Asn Gly Ser Ser Asp Gly Gly Gly Cys
20 25

<210> 213
<211> 97
<212> PRT
<213> Matrix protein M2

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Cys Arg Cys Asn Gly Ser Ser Asp Pro Leu Ala Ile Ala Ala Asn Ile
20 25 30
Ile Gly Ile Leu His Leu Ile Leu Trp Ile Leu Asp Arg Leu Phe Phe
35 40 45
Lys Cys Ile Tyr Arg Arg Phe Lys Tyr Gly Leu Lys Gly Gly Pro Ser
50 55 60
Thr Glu Gly Val Pro Lys Ser Met Arg Glu Glu Tyr Arg Lys Glu Gln
65 70 75 80
Gln Ser Ala Val Asp Ala Asp Asp Gly His Phe Val Ser Ile Glu Leu
85 90 95

Glu

<210> 214
<211> 42
<212> DNA

20870" 2060500T

<213> Oligonucleotide

<400> 214

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42

<210> 215

<211> 129

<212> PRT

<213> Bacteriophage f2

<400> 215

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Asn Val Thr Val Ala Pro Ser Asn Phe Ala Asn Gly Val Ala Glu Trp
20 25 30
Ile Ser Ser Asn Ser Arg Ser Gln Ala Tyr Lys Val Thr Cys Ser Val
35 40 45
Arg Gln Ser Ser Ala Gln Asn Arg Lys Tyr Thr Ile Lys Val Glu Val
50 55 60
Pro Lys Val Ala Thr Gln Thr Val Gly Gly Val Glu Leu Pro Val Ala
65 70 75 80
Ala Trp Arg Ser Tyr Leu Asn Leu Glu Leu Thr Ile Pro Ile Phe Ala
85 90 95
Thr Asn Ser Asp Cys Glu Leu Ile Val Lys Ala Met Gln Gly Leu Leu
100 105 110
Lys Asp Gly Asn Pro Ile Pro Ser Ala Ile Ala Ala Asn Ser Gly Ile
115 120 125

Tyr

<210> 216

<211> 17

<212> PRT

<213> Circular Mimotope

<400> 216

Gly Glu Phe Cys Ile Asn His Arg Gly Tyr Trp Val Cys Gly Asp Pro
1 5 10 15

Ala

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<210> 217

<211> 329

<212> PRT

<213> Bacteriophage Q-beta

<400> 217

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Lys	Gln	Thr	Leu	Val	Leu	Asn	Pro	Arg	Gly	Val	Asn	Pro	Thr	Asn	Gly	20	25	30	
Val	Ala	Ser	Leu	Ser	Gln	Ala	Gly	Ala	Val	Pro	Ala	Leu	Glu	Lys	Arg	35	40	45	
Val	Thr	Val	Ser	Val	Ser	Gln	Pro	Ser	Arg	Asn	Arg	Lys	Asn	Tyr	Lys	50	55	60	
Val	Gln	Val	Lys	Ile	Gln	Asn	Pro	Thr	Ala	Cys	Thr	Ala	Asn	Gly	Ser	65	70	75	80
Cys	Asp	Pro	Ser	Val	Thr	Arg	Gln	Ala	Tyr	Ala	Asp	Val	Thr	Phe	Ser	85	90	95	
Phe	Thr	Gln	Tyr	Ser	Thr	Asp	Glu	Glu	Arg	Ala	Phe	Val	Arg	Thr	Glu	100	105	110	
Leu	Ala	Ala	Leu	Leu	Ala	Ser	Pro	Leu	Leu	Ile	Asp	Ala	Ile	Asp	Gln	115	120	125	
Leu	Asn	Pro	Ala	Tyr	Trp	Thr	Leu	Leu	Ile	Ala	Gly	Gly	Gly	Ser	Gly	130	135	140	
Ser	Lys	Pro	Asp	Pro	Val	Ile	Pro	Asp	Pro	Pro	Ile	Asp	Pro	Pro	Pro	145	150	155	160
Gly	Thr	Gly	Lys	Tyr	Thr	Cys	Pro	Phe	Ala	Ile	Trp	Ser	Leu	Glu	Glu	165	170	175	
Val	Tyr	Glu	Pro	Pro	Thr	Lys	Asn	Arg	Pro	Trp	Pro	Ile	Tyr	Asn	Ala	180	185	190	
Val	Glu	Leu	Gln	Pro	Arg	Glu	Phe	Asp	Val	Ala	Leu	Lys	Asp	Leu	Leu	195	200	205	
Gly	Asn	Thr	Lys	Trp	Arg	Asp	Trp	Asp	Ser	Arg	Leu	Ser	Tyr	Thr	Thr	210	215	220	
Phe	Arg	Gly	Cys	Arg	Gly	Asn	Gly	Tyr	Ile	Asp	Leu	Asp	Ala	Thr	Tyr	225	230	235	240
Leu	Ala	Thr	Asp	Gln	Ala	Met	Arg	Asp	Gln	Lys	Tyr	Asp	Ile	Arg	Glu	245	250	255	
Gly	Lys	Lys	Pro	Gly	Ala	Phe	Gly	Asn	Ile	Glu	Arg	Phe	Ile	Tyr	Leu	260	265	270	

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Lys Ser Ile Asn Ala Tyr Cys Ser Leu Ser Asp Ile Ala Ala Tyr His
 275 280 285
 Ala Asp Gly Val Ile Val Gly Phe Trp Arg Asp Pro Ser Ser Gly Gly
 290 295 300
 Ala Ile Pro Phe Asp Phe Thr Lys Phe Asp Lys Thr Lys Cys Pro Ile
 305 310 315 320
 Gln Ala Val Ile Val Val Pro Arg Ala
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<210> 218

<211> 770

<212> PRT

<213> Amyloid-Beta Protein (Homo Sapiens)

<400> 218

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 Ala Leu Glu Val Pro Thr Asp Gly Asn Ala Gly Leu Leu Ala Glu Pro
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 Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln
 35 40 45
 Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp
 50 55 60
 Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu
 65 70 75 80
 Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn
 85 90 95
 Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val
 100 105 110
 Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu
 115 120 125
 Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys
 130 135 140
 Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu
 145 150 155 160
 Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile
 165 170 175
 Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu
 180 185 190
 Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val
 195 200 205

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Trp	Trp	Gly	Gly	Ala	Asp	Thr	Asp	Tyr	Ala	Asp	Gly	Ser	Glu	Asp	Lys
	210					215					220				
Val	Val	Glu	Val	Ala	Glu	Glu	Glu	Glu	Val	Ala	Glu	Val	Glu	Glu	Glu
225					230					235					240
Glu	Ala	Asp	Asp	Asp	Glu	Asp	Asp	Glu	Asp	Gly	Asp	Glu	Val	Glu	Glu
				245					250					255	
Glu	Ala	Glu	Glu	Pro	Tyr	Glu	Glu	Ala	Thr	Glu	Arg	Thr	Thr	Ser	Ile
			260					265					270		
Ala	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Glu	Ser	Val	Glu	Glu	Val	Val	Arg
		275					280					285			
Glu	Val	Cys	Ser	Glu	Gln	Ala	Glu	Thr	Gly	Pro	Cys	Arg	Ala	Met	Ile
	290					295					300				
Ser	Arg	Trp	Tyr	Phe	Asp	Val	Thr	Glu	Gly	Lys	Cys	Ala	Pro	Phe	Phe
305					310					315					320
Tyr	Gly	Gly	Cys	Gly	Gly	Asn	Arg	Asn	Asn	Phe	Asp	Thr	Glu	Glu	Tyr
				325					330					335	
Cys	Met	Ala	Val	Cys	Gly	Ser	Ala	Met	Ser	Gln	Ser	Leu	Leu	Lys	Thr
			340					345					350		
Thr	Gln	Glu	Pro	Leu	Ala	Arg	Asp	Pro	Val	Lys	Leu	Pro	Thr	Thr	Ala
		355					360					365			
Ala	Ser	Thr	Pro	Asp	Ala	Val	Asp	Lys	Tyr	Leu	Glu	Thr	Pro	Gly	Asp
	370					375					380				
Glu	Asn	Glu	His	Ala	His	Phe	Gln	Lys	Ala	Lys	Glu	Arg	Leu	Glu	Ala
385					390					395					400
Lys	His	Arg	Glu	Arg	Met	Ser	Gln	Val	Met	Arg	Glu	Trp	Glu	Glu	Ala
				405					410					415	
Glu	Arg	Gln	Ala	Lys	Asn	Leu	Pro	Lys	Ala	Asp	Lys	Lys	Ala	Val	Ile
			420					425					430		
Gln	His	Phe	Gln	Glu	Lys	Val	Glu	Ser	Leu	Glu	Gln	Glu	Ala	Ala	Asn
		435					440					445			
Glu	Arg	Gln	Gln	Leu	Val	Glu	Thr	His	Met	Ala	Arg	Val	Glu	Ala	Met
	450					455					460				
Leu	Asn	Asp	Arg	Arg	Arg	Leu	Ala	Leu	Glu	Asn	Tyr	Ile	Thr	Ala	Leu
465					470					475					480
Gln	Ala	Val	Pro	Pro	Arg	Pro	Arg	His	Val	Phe	Asn	Met	Leu	Lys	Lys
				485					490					495	
Tyr	Val	Arg	Ala	Glu	Gln	Lys	Asp	Arg	Gln	His	Thr	Leu	Lys	His	Phe
			500					505					510		
Glu	His	Val	Arg	Met	Val	Asp	Pro	Lys	Lys	Ala	Ala	Gln	Ile	Arg	Ser
		515					520					525			
Gln	Val	Met	Thr	His	Leu	Arg	Val	Ile	Tyr	Glu	Arg	Met	Asn	Gln	Ser
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Leu Ser Leu Leu Tyr Asn Val Pro Ala Val Ala Glu Glu Ile Gln Asp
545 550 555 560

Glu Val Asp Glu Leu Leu Gln Lys Glu Gln Asn Tyr Ser Asp Asp Val
565 570 575

Leu Ala Asn Met Ile Ser Glu Pro Arg Ile Ser Tyr Gly Asn Asp Ala
580 585 590

Leu Met Pro Ser Leu Thr Glu Thr Lys Thr Thr Val Glu Leu Leu Pro
595 600 605

Val Asn Gly Glu Phe Ser Leu Asp Asp Leu Gln Pro Trp His Ser Phe
610 615 620

Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn Glu Val Glu Pro Val
625 630 635 640

Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr Thr Arg Pro Gly Ser
645 650 655

Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser Glu Val Lys Met Asp
660 665 670

Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys Leu
675 680 685

Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile Gly
690 695 700

Leu Met Val Gly Gly Val Val Ile Ala Thr Val Ile Val Ile Thr Leu
705 710 715 720

Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile His His Gly Val Val
725 730 735

Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg His Leu Ser Lys Met
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Gln Asn
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<212> PRT

<213> Beta-Amyloid Peptide Precursor (Homo Sapiens)

<400> 219

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Met Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln
20 25 30

20250502 20250502

Lys Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile
 35 40 45
 Ile Gly Leu Met Val Gly Gly Val Val Ile Ala Thr Val Ile Ile Ile
 50 55 60
 Thr Leu Val Met Leu Lys Lys Gln Tyr Thr Ser Asn His His Gly Val
 65 70 75 80
 Val Glu

<210> 220

<211> 42

<212> PRT

<213> Amyloid Beta Peptide

<400> 220

Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys
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 20 25 30
 Gly Leu Met Val Gly Gly Val Val Ile Ala
 35 40

221:

RANKL_human: TrEMBL:O14788: extracellular domain

YFRAQMDPNRIS EDGTHCIYRI LRLHENADFQ DTTLESQDTK LIPDSCRRIK QAFQGAVQKE
 LQHIVGSQHI RAEKAMVDGS WDLAKRSKL EAQPPFAHLTI NATDIPSGSH KVSLSWYHD
 RGWAKISNMT FSNGKLIVNQ DGFYYLYANI CFRHHETSGD LATEYLQLMV YVTKTSIKIP
 SSHTLMKGGG TKYWSGNSEF HFYSINVGGF FKLRSGEEIS IEVSNPSLLD PDQDATYFGA FKVRDID

222:

RANKL_human: spliced isoformTrEMBL:O14788

MDPNRISEDG THCIYRILRL HENADFQDTT LESQDTKLIP DSCRRIKQAF QGAVQKELQH
 IVGSQHIRAE KAMVDGSWLD LAKRSKLEAQ PFAHLTINAT DIPSGSHKVS LSSWYHNRGW
 AKISNMTFSN GKLIVNQDGF YYLYANICFR HHETSGDLAT EYLQLMVYVT KTSIKIPSSH
 TLMKGGSTKY WSGNSEFHFY SINVGFFKL RSGEEISIEV SNPSLLDPDQ DATYFGAFKV
 RDID

223:

RANKL_mouse: TrEMBL:O35235: extracellular domain

YFRAQMDPNRI SEDSTHCFYR ILRLHENAGL QDSTLESED TLPDSCRRMKQ AFQGAVQKEL
 QHIVGPQRFS GAPAMMEGSW LDVAQRGKPE AQPFAHLTIN AASIPSGSHK VTLSSWYHDR

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GWAKISNMTL SNGKLRVNQD GFYYLYANIC FRHHETSGSV PTDYQLQMVY VVKTSIKIPS
SHNLMKGGST KNWSGNSEFH FYSINVG GFF KLRAGEEISI QVSNPSLLDP DQDATYFGAF KVQDID

224:

RANKL_mouse spliced isoforms: TrEMBL:Q9JJK8

MKQAFQGA VQ KELQHIVGPQ RFSGAPAMME GSWLDVAQRG KPEAQPF AHL TINAASIPSG
SHKVTLS SWY HDRGWAKISN MTL SNGKLRV NQDGFYYLYA NICFRHHETS GSVPTDYQL
MVYVVKTSIK IPSSHNLMKG GSTKNWSGNS EFHFYSINVG GFFKLRAGEE ISIQVSNPSL
LDPDQDATYF GAFKVQDID

225:

MIF_rat: SwissProt

PMFIVNTNVP RASVPEGFLS ELTQQLAQAT GKPAQYIAVH VVPDQLMTFS GTSDPCALCS
LHSIGKIGGA QNRNYSKLLC GLLSDRLHIS PDRVYINYD MNAANVGWNG STFA

226:

MIF_mouse: SwissProt

PMFIVNTNVP RASVPEGFLS ELTQQLAQAT GKPAQYIAVH VVPDQLMTFS GTNDPCALCS
LHSIGKIGGA QNRNYSKLLC GLLSDRLHIS PDRVYINYD MNAANVGWNG STFA

227:

MIF_human: SwissProt

PMFIVNTNVP RASVPDGFLS ELTQQLAQAT GKPPQYIAVH VVPDQLMAFG GSSEPCALCS
LHSIGKIGGA QNRSYSKLLC GLLAERLRIS PDRVYINYD MNAANVGWNN STFA

228:

Human IL-17

ACCESSION #: AAC50341

1 mtpgktslvs lllllsleai vkagitiprn pgcpnsedkn fprtvmvnln i hnrntntnp
61 krssdyynrs tspwnlhrne dperypsviw eakcrhl gci nadgnvdyhm nsvpiqqeil
121 vlrrepphpc nsfrlekilv svgctcvtpi vhhva

229:

Mouse IL-17

ACCESSION #: AAA37490

1 mspgrassvs lmlllllsla atvkaaa iip qssacpntea kdflqnvkvn lkvfnslgak
61 vssrpsdyl nrstspwtlh rnedpdryps viweaqcrhq rcvnaegkld hhmnsvliqq
121 eilvlkrepe scpftfrvek mlvgvgctcv asivrqaa

230:

Human IL-13 (precursor)

20050902 011002

MALLTTVIALTCLGGFASPGVPPSTALRELIEELVNITQNQKAPLCNGSMVWSINLTAGMYCAALESLINVSG
CSAIEKTQRMMSGFCPHKVSAGQFSSLHVRDTKIEVAQFVKDLLHLKKLFREGRFN

231:

Human IL-13 (processed)

GPVPPSTALR ELIEELVNIT QNQKAPLCNG SMVWSINLTA
GMYCAALES INVSGCSAIE KTQRMMSGFC PHKVSAGQFS SLHVRDTKIE VAQFVKDLLL
HLKKLFREGR FN

232:

Mouse IL-13 (processed)

GPVPRSVSLPLTLKELIEELSNIQDQTPLCNGSMVWSVDLAAGGFCVALDSLNTISNCNAIYRTQRILHGLCNR
KAPTTVSSLPDTKIEVAHFITKLLSYTKQLFRHGPF

233:

Human IL-5 (precursor)

MRMLLHLSLL ALGAAYVYAI PTEIPTSALV KETLALLSTH RTLLIANETL RIPVPVHKNH
QLCTEEIFQG IGTLESQTVQ GGTVERLFKN LSLIKKYIDG QKKKCGEERR RVNQFLDYLQEFGLGVMNTEW
IIES

234:

Human IL-5 (processed)

I PTEIPTSALV KETLALLSTH RTLLIANETL RIPVPVHKNH
QLCTEEIFQG IGTLESQTVQ GGTVERLFKN LSLIKKYIDG QKKKCGEERR RVNQFLDYLQ
EFLGVMNTEW IIES

235:

Mouse IL-5 (processed)

MEIPMSTVVKETLTQLSAHRALLTSNETMRLPVPTHKNHQLCIGEIFQGLDILKNQTVRGGTVEMLFQNLSLIKK
YIDRQKEKCGEERRRTRQFLDYLQEFGLGVMSTEWAMEG

236:

CCL21 Swissprot: SY21_human: Sequence after cleavage of signal peptide:

SDGGAQD CLKYSQRKI PAKVVRYSRK QEPSLGCSIP AILFLPRKRS QAELCADPKE LWVQQLMQHL
DKTPSPQKPA QGCRKDRGAS KTGKKGKGSK GCKRTERSQT PKGP

237:

CCL21 Swissprot: SY21_mouse: Sequence after cleavage of signal peptide:

SDGGGQD CLKYSQKKI PYSIVRGYRK QEPSLGCPIP AILFSRPHS KPCLCANPEE GWVQNLMRRL

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DQPPAPGKQS PGCRCNRGTS KSGKKGKGSK GCKRTEQTQP SRG

238:

Swissprot: SDF1_human: Sequence after cleavage of signal peptide:

DGKPVSLSYRC PCRFFESHVA RANVKHLKIL NTPNCALQIV ARLKNNNRQV CIDPKLKWIQ
EYLEKALNKR FKM

239:

Swissprot: SDF1_mouse: Sequence after cleavage of signal peptide:

DGKPVSLSYRC PCRFFESHIA RANVKHLKIL NTPNCALQIV ARLKNNNRQV CIDPKLKWIQ
EYLEKALNK

240:

BLC Sequences: Human: Accession: NP_006410

Amino acids 1-22 are signal peptide.

MKFISTSLLL MLLVSSLSPV QGVLEVYYTS LRCRCVQESS VFIPRRFIDR IQILPRGNGC
PRKEIIVWKK NKSIVCVDPQ AEWIQRMMEV LRKRSSSTLP VPVFKRKIP

241:

BLC Sequence Mouse: accession: NP_061354

Amino acids 1-21 are signal peptide

MRLSTATLLL LLASCLSPGH GILEAHYTNL KCRCSGVIST VVGLNIIDRI QVTPPGNGCP
KTEVVIWTKM KKVICVNPR KWLQRLLRHV QSKSLSSTPQ APVSKRRAA

242:

Human Eotaxin-1

1-23 is Signal peptide

1 mkvsaallwl lliaaafspq glagpasvpt tccfnlanrk iplqrlesyr ritsgkcpqk
61 avifkttklak dicadpkkkw vqdsmkyldq ksptpkp

243:

Human Eotaxin-2

1-26 is Signal peptide

1 maglmtivts llflgvcabh iiptgsvvip spccmffvsk ripenrvvsv qlssrstclk
61 agvifttkkkg qqfcgdpkqe wvqymknld akqkkaspra ravavkgpvq rypgnqtte

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244:

Human Eotaxin-3

1-23 is signal peptide

1 mmglslasav llasllslhl gtatrgsdis ktccfqyshk plpwtwvrsy eftsnscsqr
61 avifttkrqk kvcthprrkw vqkyisllkt pkql

245:

Mouse Eotaxin-1

1-23 is signal peptide

1 mqsstallfl lltvtsfts qvlahpgsipt sccfimtssk ipntllksyk ritnnrctlk
61 aivfktrlgk eicadpkkkw vqdatkhldq klqtpkp

246:

Mouse Eotaxin-2

1-25 is signal peptide

1 magsativag llllvacacc ifpidsvtip sscctsfisk kipenrvvsv qlangsicpk
61 agvifitkkg hkictdpkll wvqrhiqkld akknqpskga kavrtkfavq rrrgnstev

247:

M-CSF Sequence: human: the construct would be an N-terminal fragment consisting of residue 33 -181 or 33 -185, corresponding to the soluble form of the receptor.

Accession: NP_000748

MTAPGAAGRC PPTTWLGSLL LLVCLLASRS ITEEVSEYCS HMIGSGHLQS LQRLIDSQME
TSCQITFEFV DQEQLKDPVC YLKKAFLLVQ DIMEDTMRFR DNTPNIAIAIV QLQELSLRLK
SCFTKDYEEL DKACVRTFYE TPLQLLEKVK NVFNETKNLL DKDWNIFSKN CNNSFAECSS
QDVVTKPDCN CLYPKAIPSS DPASVSPHQP LAPSMAPVAG LTWEDSEGTE GSSLLPGEQP
LHTVDPGSAK QRPPRSTCQS FEPPETPVVK DSTIGGSPQP RPSVGAFNPG MEDILDSAMG
TNWVPEEASG EASEIPVPQG TELSPSRPGG GSMQTEPARP SNFLSASSPL PASAKGQOPA
DVTGTALPRV GPVRPTGQDW NHTPQKTDHP SALLRDPPEP GSPRISSPRP QGLSNPSTLS
AQPQLSRSHS SGSVLPLGEL EGRRSTRDRR SPAEPEGGPA SEGAARPLPR FNSVPLTDTH
ERQSEGSSSP QLQESVFHLL VPSVILVLLA VGGLLFYRWR RRS HQEPQRA DSPLEQPEGS
PLTQDDRQVE LPV

248:

M-CSF Mouse sequence: Mature sequence starts at amino acid 33. Accession. NP_031804

MTARGAAGRC PSSTWLGSRL LLVCLLMSRS IAKEVSEHCS HMIGNHGLKV LQQLIDSQME
TSCQIAFEFV DQEQLDDPVC YLKKAFLLVQ DIIDETMRFK DNTPNANATE RLQELSNNLN
SCFTKDYEEL NKACVRTFHE TPLQLLEKIK NFFNETKNLL EKDWNIFTKN CNNSFAKCSS
RDVVTKPDCN CLYPKATPSS DPASASPHQP PAPSMAPLAG LAWDDSQRTE GSSLLPSELP
LRIEDPGSAK QRPPRSTCQT LESTE QPNHG DRLTEDSQPH PSAGGPVPGV EDILESSLGT
NWLLEEASGE ASEGFLTQEA KFSPSTPVGG SIQAETDRPR ALSASPFPKS TEDQKPV DIT

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DRPLTEVNPM RPIGQTQNNNT PEKTDGTSTL REDHQEPGSP HIATPNPQRV SNSATPVAQL
LLPKSHSWG I VLPLGELEGK RSTRDRRSPA ELEGGSASEG AARPVARFNS IPLTDTGHVE
QHEGSSDPQI PESVFHLLVP GIILVLLTVG GLLFYKWKWR SHRDPQTLDS SVGRPEDSSL
TQDEDRQVEL PV

249:

Sequence of Human Resistin: Precursor.

MKALCLLLLPLVLGLLVSSKTLCSMEEAINERIQEVAGSLIFRAISSIGLECQSVTSRGDLATCPRGFAVTGCTCG
SACGSWDVRAETTHCQCAGMDWTGARCCRVQP

250:

Sequence of Mouse Resistin: Precursor.

MKNLSFPLLFLFFLVPELLGSSMPLCPIDEAIDKKIKQDFNSLFPNAIKNIGLNCWTVSSRGKLASCPEGTAVLSCSC
GSACGSWDIREEKVCHCQCARIDWTAARCCCKLQVAS

251:

Lymphotoxin- β :

Swissprot: TNFC_human: Sequence of the extracellular domain:

QD QGGLVTETAD PGAQAQQLG FQKLPEEEPE TDLSPGLPAA HLIGAPLKGQ GLGWETTKEQ
AFLTSGTQFS DAEGALPQD GLYYLYCLVG YRGRAPPGGG DPQGRSVTLR SSLYRAGGAY GPGTPELLLE
GAETVTPVLD PARRQYGPL WYTSVGFGGL VQLRRGERVY VN

252:

Lymphotoxin- β :

Swissprot: TNFC_mouse: Sequence of the extracellular domain:

QD QGRRVEKIIG SGAQAQKRLD DSKPSCILPS PSSLSETPDP RLHPQRSNAS RNLASTSQGP
VAQSSREASA WMTILSPAAD STPDPGVQQL PKGEPETDLN PELPAAHLIG AWMSGQGLSW
EASQEEAFRL SGAQFSPTHG LALPDQGVYY LYCHVGYRGR TPPAGRSRAR SLTLRSALYR
AGGAYGRGSP ELLLEGAETV TPVVDPIGYG SLWYTSVGFG GLAQLRSGER VYVNISHPDM
VDYRRGKTFF GAVMVG

253:

RNA-phage PP7:

msktivlsvg eatrtlteiq stadrqifee kvgplvgrlr ltaslrqnga ktayrvnlkl
dqadvdcst svcgelpkvr ytgwshdvt ivansteasr kslydltksl vatsqvedlv
vnlvplgr

254:

RNA-phage SP A1 protein:

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aklnqvtls kigkngdqt1 tltprgvnpt ngvaslseag avpalekrvt vsvaqpsrnr
knfkvqiklq nptactrdac dpsvtrsafa dvtslftsyst tdeeralirt elaalladpl
ivdaidnlnp aywaallvas sgggdnpdp dvppvdpvkp pdgtgrykcp facyrlgsiy
evgkegsdip yergdevsvt fdyaedflg ntnwrnwdqr lsdydianrr rcrngnyidl
datamqsddf vlsgrgyvrk vkfpgafgsi kyllniqgda wldlsevtay rsygmvigfw
tdskspqlpt dftqfnsanc pvqtviiips 1

255:

"Qβ 240":

AKLETVTTLGNIG**RD**GKQTLVLNPRGVNPTNGVASLSQAGAVP
ALEKRVTVSVSQPSRNRKQYKVQVKIQNPTACTANGSCDPSVTRQ
KYADVTFSTQYSTDEERAFVRTELAALLASPLLIDAIDQLNPAY

256:

"Qβ 243":

AKLETVTTLGKIGKD**G**KQTLVLNPRGVNPTNGVASLSQAGAVP
ALEKRVTVSVSQPSRNRKQYKVQVKIQNPTACTANGSCDPSVTRQ
KYADVTFSTQYSTDEERAFVRTELAALLASPLLIDAIDQLNPAY

257:

"Qβ 250":

ARLETVTTLGNIG**RD**GKQTLVLNPRGVNPTNGVASLSQAGAVP
ALEKRVTVSVSQPSRNRKQYKVQVKIQNPTACTANGSCDPSVTRQ
KYADVTFSTQYSTDEERAFVRTELAALLASPLLIDAIDQLNPAY

258:

"Qβ 259":

ARLETVTTLGNIGKDGRQTLVLNPRGVNPTNGVASLSQAGAVP
ALEKRVTVSVSQPSRNRKQYKVQVKIQNPTACTANGSCDPSVTRQ
KYADVTFSTQYSTDEERAFVRTELAALLASPLLIDAIDQLNPAY

259:

"Qβ 251":

AKLETVTTLGNIGKDGRQTLVLNPRGVNPTNGVASLSQAGAVP
ALEKRVTVSVSQPSRNRKQYKVQVKIQNPTACTANGSCDPSVTRQ
KYADVTFSTQYSTDEERAFVRTELAALLASPLLIDAIDQLNPAY

260:

PH19 (SEQ ID NO:260)

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TAAGTCCTCTGCCACGTACC

261:

PH20 (SEQ ID NO:261)

TGGAAACCACGCTCACTTCC

262:

PH21 (SEQ ID NO:262)

CGGGATCCGGGATGAAGAACCTTTCATTTC

263:

PH22 (SEQ ID NO:263)

GCCTCTAGAGAGGAAGCGACCTGCAGCTTAC

264:

PH29 (SEQ ID NO:264)

CTAGCGGGAGGGGGTGGATGTGGGGACGACTACAAGGATGACGACA

265:

PH30 (SEQ ID NO:265)

AGCTTGTCGTCATCCTTGTAAGTCGTCCCCACATCCACCCCCTCCCG

266:

PH31 (SEQ ID NO:266)

AGCTTACTCACACATGCCCACCGTGCCCAGCACCTGAAGCCGAGG

267:

PH32 (SEQ ID NO:267)

CGGCTTCAGGTGCTGGGCACGGTGGGCATGTGTGAGTA

268:

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208TF0" 20650500T

PH35 (SEQ ID NO:268)

CTAGCGGGAGGGGGTGGATGTGGGATCGAAGGTCGCA

269:

PH36 (SEQ ID NO:269)

AGCTTGCGACCTTCGATCCCACATCCACCCCCTCCCG

270:

PH37 (SEQ ID NO:270)

CGGGATCCAGCAGCTGGGCTCGAGGTGCTAGCTTTGTTTAAAC

271:

PH38 (SEQ ID NO:271)

GATCGTTTAAACAAACAAAGCTAGCACCTCGAGCCCAGCTGCTGGATCCCGGTAC

272:

PH39 (SEQ ID NO:272)

CTAGCGGGAGGGGGTGGATGTGGGGACGATGACGACA

273:

PH40 (SEQ ID NO:273)

AGCTTGTCGTCATCGTCCCCACATCCACCCCCTCCCG

274:

PH41 (SEQ ID NO:274)

CATGGAGACAGACACACTCCTGCTATGGGT

275:

PH42 (SEQ ID NO:275)

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GCAGTACCCATAGCAGGAGTGTGTCTGTCTCCATGGTAC

276:

PH43 (SEQ ID NO:276)

ACTGCTGCTCTGGGTTCCAGGTTCCACTGGTGACGCG

277:

PH44 (SEQ ID NO:277)

GATCCGCGTCACCAGTGGAACCTGGAACCCAGAGCA

278:

SU7 (SEQ ID NO:278)

AGCTTGCGGATCCAGGATATCGGCTCGAGGTTCTAGAGTG

279:

SU8 (SEQ ID NO:279)

GGCCCACTCTAGAACCTCGAGCCGATATCCTGGATCCGCA

280:

Resistin-C-Xa:

SSMPLCPIDEAIDKKIKQDFNSLFPNAIKNIGLNCWTVSSRGKLASCPEGTAVLSCSCG
SACGSWDIREEKVCHCQCARIDWTAARCKLQVASSLAGGGGCGIEGR

281:

Resistin-C-EK

SSMPLCPIDEAIDKKIKQDFNSLFPNAIKNIGLNCWTVSSRGKLASCPEGTAVLSCSCG
SACGSWDIREEKVCHCQCARIDWTAARCKLQVASSLAGGGGCGDDDD

282:

Resistin-GCG:

SSMPLCPIDEAIDKKIKQDFNSLFPNAIKNIGLNCWTVSSRGKLASCPEGTAVLSCSCG
SACGSWDIREEKVCHCQCARIDWTAARCKLQVASSLAGGGGCG

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283:

pCep-Xa-Fc*: (complete sequence)

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1  GCCCCGCCGC CGGACGAACT AAACCTGACT ACGGCATCTC TGCCCCCTCT TCGCTGGTAC GAGGAGCGCT
71  TTTGTTTTGT ATTGGGGGCA GTGCATGTAA TCCCTTCAGT TGTTTGGTAC AACTTGCCAA CTGGGCGCTG
141  TTCCACATGT GACACGGGGG GGGACCAAAC ACAAGGGGT TCTCTGACTG TAGTTGACAT CCTTATAAAT
211  GGATGTGCAC ATTTGCCAAC ACTGAGTGGC TTTCATCCTG GAGCAGACTT TGCATGCTGT GGACTGCAAC
281  ACAACATTGC CTTTATGTGT AACTCTTGGC TGAAGCTCTT ACACCAATGC TGGGGGACAT GTACCTCCCA
351  GGGGCCAGG AAGACTACGG GAGGCTACAC CAACGTCAAT CAGAGGGGCC TGTGTAGCTA CCGATAAGCG
421  GACCCTCAAG AGGGCATTAG CAATAGTGT TAACCTAAT TCAATAGCAT ATGTTACCCA ACGGGAAGCA
491  TTCCCGGGTA GTAGTATATA CTATCCAGAC TAACCTAAT TCAATAGCAT ATGTTACCCA ACGGGAAGCA
561  TATGCTATCG AATTAGGGTT AGTAAAAGGG TCCTAAGGAA CAGCGATATC TCCACCCCA TGAGCTGTCA
631  CGGTTTTATT TACATGGGGT CAGGATTCCA CGAGGGTAGT GAACCATTTT AGTCACAAGG GCAGTGGCTG
701  AAGATCAAGG AGCGGGCAGT GAACCTCTCT GAATCTTCGC CTGCTCTCTC ATTCTCCTTC GTTTAGCTAA
771  TAGAATAACT GCTGAGTTGT GAACAGTAAG GTGTATGTGA GGTGCTCGAA AACAAGGTTT CAGGTGACGC
841  CCCCAGAATA AAATTTGGAC GGGGGTTTCA GTGGTGGCAT TGTGCTATGA CACCAATATA ACCCTCACAA
911  ACCCTTGGG CAATAAATAC TAGTGTAGGA ATGAAACATT CTGAATATCT TTAACAATAG AAATCCATGG
981  GGTGGGGACA AGCCGTAAAG ACTGGATGTC CATCTCACAC GAATTTATGG CTATGGGCAA CACATAATCC
1051  TAGTGCAATA TGATACTGGG GTTATTAAGA GTGGTGGCAT TGTGCTATGA CACCAATATA ACCCTCACAA
1121  TACACTCTAT TTGTAACAAG GGGAAAGAGA GTGGACGCGG ACAGCAGCGG ACTCCACTGG TGTCTCTTAA
1191  CACCCCGGAA AATTAAACGG GGTCCACGCG CAATGGGGCC CATAAACAAA GACAAGTGGC CACTCTTTTT
1261  TTTGAAATTG TGGAGTGGGG GCACGCGTCA GCGCCACAC GCGGTCAAAC CACTTGCCCA CAAAACCACT
1331  GGGTGTAATA ACTTGGCTGA TTGTAACCCC GCTAACCCTG GCGGTCAAAC CACTTGCCCA CAAAACCACT
1401  AATGGCACCC CGGGGAATAC CTGCATAAGT AGGTGGGCGG GCCAAGATAG GGGCGCGATT GCTGCGATCT
1471  GGAGGACAAA TTACACACAC TTGCGCCTGA GCGCCAAGCA CAGGTTGTTT GGTCTCTATA TACACGAGT
1541  CGCTGAGAGC ACGGTGGGCT AATGTTGCCA TGGGTAGCAT ATACTACCCA AATATCTGGA TAGCATATGC
1611  TATCCTAATC TATATCTGGG TAGCATAGGC TATCCTAATC TATATCTGGG TAGCATATGC TATCCTAATC
1681  TATATCTGGG TAGTATATGC TATCCTAATC TATATCTGGG TAGCATATGC TATCCTAATC TATATCTGGG
1751  TAGCATATGC TATCCTAATC TATATCTGGG TAGTATATGC TATCCTAATC TATATCTGGG TAGCATATGC
1821  TATCCTAATA GAGATTAGGG TAGTATATGC TATCCTAATC TATATCTGGG TAGCATATGC TATCCTAATC
1891  TCTGGATAGC ATATGCTATC CTAATCTATA TCTGGGTAGC ATATGCTATC CTAATCTATA TCTGGGTAGC
1961  ATAGGCTATC CTAATCTATA TCTGGGTAGC ATATGCTATC CTAATCTATA TCTGGGTAGC ATATGCTATC
2031  CTAATTTATA TCTGGGTAGC ATAGGCTATC CTAATCTATA TCTGGGTAGC ATATGCTATC CTAATCTATA
2101  TCTGGGTAGT ATATGCTATC CTAATCTATA TCTGGGTAGC ATATGCTATC CTAATCTATA TCTGGGTAGC
2171  ATATGATACC CAGTAGTAGA GTGGGAGTGC TATCCTTTGC ATATGCTATC CTAATCTATA TCTGGGTAGC
2241  TTTTCGCTGC TTGTCCTTTT CCTGCATGCT GGTGCTCCC ATTCTTAGGT GAATTTAAGG AGGCCAGGCT
2311  AAAGCCGTCG CATGCTCGAT TGCTCACCAG GTAAATGTCG CTAATGTTT CCAACGCGAG AAGGTGTTGA
2381  GCGCGGAGCT GAGTGACGTG ACAACAGTGG ATATGCCAAT TGCCCCATGT TGGGAGGACG AAAATGGTGA
2451  CAAGACAGAT GGCCAGAAAT ACACCAACAG CACGCATGAT GTCTACTGGG GATTATTCTT TTAGTGCGGG
2521  GGAATACACG GCTTTTAATA CGATTGAGGG CGTCTCCTAA CAAGTTACAT CACTCCTGCC CTCTCCTACC
2591  CTCATCTTCA TCACCTCCTT CATCTCCGTC ATCTCCGTC TACCCCTCCG TCACCCCTCC GAGTTTATTCT
2661  GGTGGAAACC AGGGAGGCAA ATCTACTCCA TCGTCAAAGC TGCACACAGT CACCCTGATA TTGACAGTAA
2731  GAGCGGGCTT GTGCATAACA AGGTCTCTAA TCGCATCTCT CAAACCTCA GCAAATATAT GAGTTGTAG
2801  AAAGACCATC AAATAACAGA CAATGGACTC TATGCCCGGG CCAGGTTGTG GGCCGGGTCC AGGGGCCATT
2871  CCAAAGGGGA GACGACTCAA TGGTGTAAAG CGACATTGTG GAATAGCAAG GGCAGTTCTT CGCCTTAGGT
2941  TGTAAGGGGA GGTCTTACTA CCTCCATATA CGAACACACC GGCAGCCCAA GTTCTCTCGT GGTGGAACCT
3011  TTCTCAGTGA CTTCTAGCCA CTTCTAGCGG CTTTAGCGGG CAGGTTGTG GGCCGGGTCC AGGGGCCATT
3081  CCTTGACCAC GATGCTTTCC AAACCACCT CTTTCTTTGC GCCTGCCTCC ATCACCCTGA CCCCAGGCTC
3151  CAGTGCTTGG GCCTTCTCCT GGGTCATCTG CCGGGCCCTG CTCTATCGCT CCCGGGGGCA CGTCAGGCTC
3221  ACCATCTGGG CCACCTTCTT GGTGGTATTC AAAAATATCG GCTTCCCCTA CAGGGTGGAA AAATGGCCTT
3291  CTACCTGGAG GGGGCTGCG CGGTGGAGAC CCGGATGATG ATGACTGACT ACTGGGACTC CTGGGCTCTT
3361  TTTCTCCACG TCCACGACCT CTCCCCTTGG CTCTTTTACG ACTTCCCCC CTGGCTCTTT CACGTCCTCT
3431  ATCCCGGCGG CCTCCACTAC CTCCTCGACC CCGGCCCTCA CTACCTCCTC GACCCCGGCC TCCACTGCCT
3501  CCTCGACCCC GGCCTCCACC TCCTGCTCCT GCCCCTCTCG CTCCTGCCCC TCCTCTGCTC CTGCCCCCTC
3571  CTGCCCCCTC TCTCCTTGCC CCTCCTGCCC TCCTGCTCCT TGCCCCCTCT GCCCCCTCTG CTCCTGCCCC
3641  TCCTGCCCCC CCTCCTGCTC CTGCCCCCTC TGCCCCCTCT GCCCCCTCTG CCCCCTCTGC CCTCCTGCTC
3711  CCTGCCCCCT CTGCCCCCTC TGCTCCTGCC CCTCCTGCCC CTCCTGCTCC TGCCCCCTCT GCTCCTGCTC
3781  CTCCTGCTCC TGCCCCCTCT GCTCCTGCCC CTCCTGCCCC TCCTGCCCCC CCTCCTGCTC CTGCCCCCTC
3851  TGCTCCTGCC CTTCTGCCC CTCCTGCCCC TCCTGCTCCT GCCCCCTCTC CTGCTCCTGC CCTCCTGCTC
3921  CTCCTGCCCC CTCCTCCTGC TCCTGCCCCC CCTGCCCCC CTCCTGCTCC TGCCCCCTCT CCTCCTGCTC
3991  CCCCCTCTGC CCCCCTGCCC CTCCTCCTGC CTCCTGCCCC TCCTGCCCCC CCTCCTGCTC CTGCCCCCTC
4061  TCCTGCTCCT GCCCCCTCTG CCCCCTCTGC CCCCCTCTCT GCTCCTGCCC CTCCTCCTGC CTCCTCCTGC
4131  CCTGCCCCCT CTGCCCCCTC TGCCCCCTCT CCGTCTCTG CCCCCTCTCC TGCTCCTGCC CCTCCTGCTC
4201  CTGCCCCCTC CGCTCTGCTC CCGTCTCTG TTTCCACGTG GGTCCCCTTG CAGCCAATGC AACTTGGACG
4271  TTTTGGGGT TCCCGGACAC CATCTCTATG TCTTGGCCCT GGTATATACC CCCTCTCTT TGAGGTCCAC
4341  CCGCCTCCTC GTCCTCGTCC TCTTCCCGCT CCTCGTCCAT GGTATATACC CCCTCTCTT TGAGGTCCAC
4411  TGCCCGCGGA GCCTTCTGGT CCAGATGTGT CTCCCCTCTC TCCTAGGCCA TTTCCAGGTC CTGACTCTGG
4481  CCCCTCGTCA GACTCCTGTC CCCCTCCAAC AGCCCCCCTA CCCTCATCCC TTCTATGGTC GCTGTAGAC
4551  CAGGAGTGC AGACTCCTGC CCCCTCCAAC AGCCCCCCTA CCCTCATCCC TTCTATGGTC GCTGTAGAC
4621  AGATCCAGGT CTGAAAATTC CCCATCTCTC GAACCATCTC CGTCTCTATC ACCAATTACT CGCAGCCCGG
4691  AAAACTCCCG CTGAACATCC TCAAGATTGT CCGCTGAGC CTCAAGCCAG GCCTCAAATT CCGTCTCTCC
4761  CTTTTTGTCT GACGGTAGGG ATGGGGATTC TCGGGACCCC TCCTCTCTCT CTCAAGGTC ACCAGACAGA
4831  GATGCTACTG GGGCAACGGA AGAAAAGCTG GGTGCGCCT GTGAGGATCA GCTTATCGAT GATAAGCTGT

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4901 CAAACATGAG AATTCTTGAA GACGAAAGGG CCTCGTGATA CGCCTATTTT TATAGGTAA TGTCATGATA
4971 ATAATGGTTT CTTAGACGTC AGGTGGCACT TTTCGGGGAA ATGTGCGCGG AACCCCTATT TGTATTATTT
5041 TCTAAATACA TTCAAATATG TATCCGCTCA TGAGACAATA ACCCTGATAA ATGCTTCAAT AATATTGAAA
5111 AAGGAAGAGT ATGAGTATTC AACATTTCCTG TGTCGCCCTT ATTCCTTTT TTGCGGCATT TTGCCTTCCT
5181 GTTTTTGCTC ACCCAGAAAC GCTGGTGAAA GTAAAAGATG CTGAAGATCA GTTGGGTGCA CGAGTGGGTT
5251 ACATCGAACT GGATCTCAAC AGCGGTAAGA TCCTTGAGAG TTTTCGCCCC GAAGAACGTT TTCCAATGAT
5321 GAGCACTTTT AAAGTTCTGC TATGTGGCGC GGTATTATCC CGTGTGACG CCGGGCAAGA GCAACTCGGT
5391 CGCCGCATAC ACTATTCTCA GAATGACTTG GTTGAGTACT CACCAGTCAC AGAAAAGCAT CTTACGGATG
5461 GCATGACAGT AAGAGAATTA TGCAGTGTCT CCATAACCAT GAGTGATAAC ACTGCGGCCA ACTTACTTCT
5531 GACAACGATC GGAGGACCGA AGGAGCTAAC CGCTTTTTTG CACAACATGG GGGATCATGT AACTCGCCTT
5601 GATCGTTGGG AACCGGAGCT GAATGAAGCC ATACCAAACG ACGAGCGTGA CACCACGATG CCTGCAGCAA
5671 TGGCAACAAC GTTGCACAAA CTATTAACCT GCGAAGTACT TACTCTAGCT TCCCGGCAAC AATTAATAGA
5741 CTGGATGGAG GCGGATAAAG TTGCAGGACC ACTTCTGCGC TCGGCCCTTC CGGCTGGCTG GTTTATTGCT
5811 GATAAATCTG GAGCCGGTGA GCGTGGGTCT CGCGGTATCA GCGGTATGTA TATGGATGAA CGAAATAGAC AGATCGCTGA
5881 CCGGTATCGT AGTTATCTAC ACGACGGGGA CTGAGGCAAC TAGGTTACT CATATATACT TTAGATTGAT
5951 GATAGGTGCC TCACTGATTA AGCATTGGTA ACTGTCAGAC CAAGTTTACT CATATATACT TTAGATTGAT
6021 TTAAAACCTT ATTTTAAATT TAAAAGGATC TAGGTGAAGA TCCTTTTGTG TAATCTCATG ACCAAAATCC
6091 CTTAACTGTA GTTTTCGTTC CACTGAGCGT CAGCCCCGT AGAAAAGATC AAAGGATCTT CTTGAGATCC
6161 TTTTTTCTG CGCGTAATCT GCTGCTTGCA AACAAAAAAA CCACCGCTAC CAGCGGTGGT TGTGTTGCGC
6231 GATCAAGAGC TACCAACTCT TTTTCCGAAG GTAACCTGGT TCAGCAGAGC GCAGATACCA AATACTGTCC
6301 TTCTAGTGTG GCCGTAGTGA GGCCACCAT TCAAGAAGTC TGTAGCACC CGTACATACC TCGCTCTGCT
6371 AATCCTGTTA CAGTGGCTG CTGCCAGTGG CGATAAGTCG TGTCTTACCG GGTGAGACTC AAGACGATG
6441 TTACCGGATA AGGCGCAGCG GTCCGGGCTGA ACGGGGGGTT CGTGACACA GCCCAGCTTG GAGCGAACGA
6511 CCTACACCGA ACTGAGATAC CTACAGCGTG CTACAGCTGA AAGCGCCACG CTTCCCGAAG GAGAGAAAGC
6581 GGACAGGTAT CCGGTAAGCG GCAGGGTCCG AACAGGAGAG CGCACGAGGG AGCTTCCAGG GGGAAACGCC
6651 TGGTATCTTT ATAGTCTCTG CCGGTTTCGC CACCTCTGAC TTGAGCGTGC ATTTTGTGA TGCTCGTCAG
6721 GGGGGCGGAG CCTATGGAAA AACCGCAGCA ACGCGGCCCT TTTACGGTTC CTGCGCTTTT GCTGCGCCGC
6791 GTGCGGCTGC TGGAGATGGC GGACGCGATG GATATGTTCT GCCAAGGGTT GGTGTCGCA TTCACAGTTC
6861 TCCGCAAGAA TTGATTGGCT CCAATTCCTG GAGTGGTGAA TCCGTTAGCG AGGCCATCCA GCCTCGGCTC
6931 GAACATAGTG ATCCGCTGTG GAATGTGTGT CAGTTAGGTT GTGGAAAGTC CCCAGGCTCC CCAGCAGGCA
7001 GAAGTATGCA AAGCATGCAT CTCATATTAG CAGCAACCAG GTGTGGAAG TCCCAGGCT CCCAGCAGG
7071 CAGAAGTATG CAAAGCATGC ATCTCAATTA GTCAGCAACC ATAGTCCCGC CCTAACTCC GCCCATCCCG
7141 CCCTAACTC GCGCCAGTTC CGCCCACTCT GAGCTATTCC AGAAGTAGTG AGGAGGCTTT TTTGGAGGTT GACCGCCACG
7211 CCGAGGCCGC CTCGGCCTCT CTGACCCACG CCGCTGACCC CTCACAAGGA GACGACCTTC CATGACCGAG
7281 ACCGGTGCCG CCAGCATCCC CTGACCCACG CCGCGGCTCC CCGGGGCCGT ACGCACCTCC CGCGCCGCGT
7351 TACAAGCCCA CGTGGCGCCT CGCCACCCGC CAGCAGCTCC CCGGCCACATC GAACGCGTCA CCGAGCTGCA
7421 TCGCCGACTA CCGCGCACG CGCCACACCG TCGACCCCGA CCGCCACATC GAACGCGTCA CCGAGCTGCA
7491 AGAAGTCTTC CTCACGCGCG TCGGGCTCGA CATCGGCAAG GTGTGGGTCG CGGACGACGG CGCCGCGGTG
7561 GCGGCTCTGT CACGCGCGA GAGCGTCGAA GCGGGGGCGG TGTTCGCGGA GATCGGGCCG CGCATGGCCG
7631 AGTTGAGCGG TTCCCGGCTG GCCGCGCAGC AACAGATGGA AGGCCTCCTG GCGCGCACG GGGCCAAGGA
7701 GCGCGCGTGG TTCTTGCCCA CCGTCGGCGT CTCGCGCCG CACCAGGGCA AGGGTCTGGG CAGCGCCGTC
7771 GTGCTCCCGG GAGTGGAGGC GCGCGAGCGC GCGGGGGTGC CCGCCTTCCT CCGCCTTCCT GGAGACCTCC GCGCCCGCGA
7841 ACCTCCCTTT CTACGAGCGG CTCGGCTTCA CCGTCACCGC CGAGCTCGAG TGCCCGAAG ACCGCGCGAC
7911 CTGCTGCTAT ACCCGCAAGC CCGGTGCTG ACGCCCGCCC CACGACCCGC AGCGCCCGAC CGAAAGGAGC
7981 GCGAGCAGCG GTCCGACGGC GCGCCACGGG TCCAGGGGG GTGCGACCTCG AAACCTGTTT ATTCGACCTG
8051 ATAATGGTTA CAAATAAAGC AATAGCATCA CAAATTTTCA AATAAAGCA TTTTTCCTAC TGCATTCTAG
8121 TTGTGGTTTG TCCAAACTCA TCAATGTATC TTATCATGTC TGGATCGATC CGAACCCCTT CCTCGACCAA
8191 TTCTCATGTT TCAGACCTTA TCATCGCAGA TCCGCGCAAC GTTGTGTCAT TGCTGCAGGC CGATAGCTGG
8261 TAGGTATGGA AGATCTATAC ATTGAATCAA TATTGGCAAT TAGCCATATT AGTCATTGGT TATATAGCAT
8331 AAATCAATAT TGGCTATTGG CCATTGCATA CGTTGTATCT ATATCATAAT ATGTACATTT ATATTGGCTC
8401 ATGTCCCAAT TGACCGCCAT GTTGACATTG ATTTATGACT AGTTATTAAT AGTAATCAAT TACGGGTGCA
8471 TTAGTTCATA GCGCATATAT GGAGTTCCGC GTTACATAAC TTACGGTAAA TGGCCCGCCT GGCTGACCGC
8541 CCAACGACCC CGCGCCATTG ACGTCAATAA TGACGTATGT TCCCATAGTA ACGCCAATAG GGACTTTCCA
8611 TTGACGTCAA TGGGTGGAGT ATTTACGGTA AACTGCCCCA TTGGCAGTAC ATCAAGTGTA TCATATGCCA
8681 AGTCCGCCCC CTATTGACGT CAATGACGGT AAATGGCCCG CCTGGCATTG TGCCAGTAC ATGACCTTAC
8751 GGGACTTTTC TACTTGGCAG TACATCTACG TATTAGTCAT CGCTATTACC ATGGTGATGC GGTTTTGGCA
8821 GTACACCAAT GGGCGTGGAT AGCGGTTTGA CTCACGGGGA TTTCCAAGTC TCCACCCCAT TGACGTCAAT
8891 GGGAGTTTGT TTTGGCACCA AAATCAACGG GACTTTCCAA AATGTCGTAA TAACCCCGCC CCGTTGACGC
8961 AAATGGGCGG TAGGCGTGTA CCGTGGGAGG TCTATATAAG CAGAGCTCGT TTAGTGAACC GTCAGATCTC
9031 TAGAAGCTGG GTACCGGGAT CCAGCAGCTG GGTTCGAGGT GCTAGCGGGA GGGGGTGGAT GTGGGATCGA
9101 AGGTCGCAAG CTTACTCACA CATGCCACC GTGCCAGCA CCTGAAGCCG AGGGGGCACC GTCAGTCTTC
9171 CTCTTCCCCC CAAAACCCAA GGACACCCCT ATGATCTCCC GGACCCCTGA GGTACATGTC GTGTGTTGG
9241 ACGTGAGCTA CGAAGACCTT GAGGTCAAGT TCAACTGGTA CGTGGACGGC GTGGAGGTGC ATAATGCCAA
9311 GACAAAGCCG CGGGAGGAGC AGTACAACAG CACGTACCGT GTGGTCAGCG TCCTCACCCT CCTGCACCAG
9381 GACTGGCTGA ATGGCAAGGA GTACAAGTGC AAGGTCTCCA ACAAGCCCTT CCCAGCCTCC ATCGAGAAAA
9451 CCATCTCCAA AGCCAAAGGG CAGCCCGAG CAGCCAGGT GTACACCTG CCCCATCCC GCGACATCGC CGTGGAGTGG
9521 GACCAAGAAC CAGGTCAGCC TGACCTGCCT GGTCAAAGGC TTCTATCCCA GCGACATCGC CGTGGAGTGG
9591 GAGAGCAATG GGCAGCCGGA GAACAACACT AAGACACCGC CTCCTGTTGT GAGACTCCGAC GGCTCCTTCT
9661 TCCTCTACAG CAAGCTCACC GTGGACAAGA GCAGGTGGCA TCCCTGTCTC CCGGTAAATG ACTCGAGGCC
9731 GCATGAGGCT CTGCAACAAC ACTACACGCA GAAGAGCCTC TCCCTGTCTC GTCGACCATC ATCATCATCA TCATTGAGTT
9801 CGAACAAAAA CTCATCTCAG AAGAGGATCT GAATAGCGCC GTCCAGCATC ACAAACCACT AGTAGAATGC AGTGAAGAAA
9871 TNAACGATCC AGACATGATA AGATACATTG ATGAGTTTGG TGTCTTATTT GTAACCATTA TAAGCTGCAA TAAACAAGTT
9941 ATGCTTTATT TGTGAAATTT GTGATGCTAT TGCTTTATTT GAGGTTTGGG GAGGTTTGGG GAGGTTTGGG GAGGTTTGGG
10011 AACAACAACA ATTGCATTCA TTTTATGTTT CAGGTTTCAGG GGGAGGTGGG GAGGTTTGGG GAGGTTTGGG GAGGTTTGGG
10081 AAACCTCTAC AAATGTGGTA TGGCTGATTA TGATCCGGCT TCTGTAAGCG GATGCCGGGA GCAGACAAGC
10151 ACCTCTGACA CATGCAGCTC CCGGAGACGG TCACAGCTTG TCTGTAAGCG GATGCCGGGA GCAGACAAGC
10221 CCGTCAGGGC GCGTCAGCGG GTGTTGGCGG GTGTCGGGGC GCAGCATAGA CCGGTCGACT CTAGA
```

284:

5'LT• : (SEQ ID NO:284)

5'-CTT GGT GCC GCA GGA TCA G-3'

285:

3'LT• : (SEQ ID NO:285)

5'-CAG ATG GCT GTC ACC CCA C-3'

286:

5'LT• long-*NheI*: (SEQ ID NO:286)

5'-GCC CGC TAG CCT GCG GTG GTC AGG ATC AGG GAC GTC G-3'

287:

5'LT• short-*NheI*: (SEQ ID NO:287)

5'-GCC CGC TAG CCT GCG GTG GTT CTC CAG CTG CGG ATT C -3'

288:

3'LT• stop-*NotI*: (SEQ ID NO:288)

5'-CAA TGA CTG CGG CCG CTT ACC CCA CCA TCA CCG -3'

289:

GST-EK-C-LT•₄₉₋₃₀₆: SEQ ID NO:289

APLVMSPILGYWKIKGLVQPTRLLEYLEEKYEEHLYERDEGDKWRNKKFELGLEFPNLPYYIDGDVKLTQ
SMAIIRYIADKHNMLGGCPKERAIEISMLEGAVLDIRYGVSRAYSDFETLKVDFLSKLPEMLKMFEDRLCH
KTYLNGDHVTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIQIDKYLKSSKYIAWPLQGWQATF
GGGDHPPKASMTGGQQMGRDLYDDDDKLACGGQDQGRRVEKIIIGSGAQAQKRLDDSKPSCILPSPSSL
SETPDPRLHPQRSNASRNLASTSQGPVAQSSREASAWMTILSPAADSTPDGPVQQLPKGEPETDLNPEL
PAAHLIGAWMSGQGLSWEASQEEAFLRSGAQFSPTHGLALPQDGVVYLYCHVGYRGRTPPAGRSRARS
LTLRSALYRAGGAYGRGSPELLLEGAETVTPVVDPIGYGSLWYTSVGFGGLAQLRSGERVVYNISHPDMV
DYRRGKTFFGAVMVG

290:

GST-EK-C-LT•₁₂₆₋₃₀₆: SEQ ID NO:290

20250902 01:00:20

APLVMSPILGYWKIKGLVQPTRLLLEYLEEKYEEHLYERDEGDKWRNKKFELGLEFPNLPYYIDGDVKLTQ
SMAIIRYIADKHNMLGGCPKERAISMLEGAVLDIRYGVSRAYSKDFETLKVDFLSKLPEMLKMFEDRLCH
KTYLNGDHVTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIQIDKYLKSSKYIAWPLQGWQATF
GGGDHPPKASMTGGQQMGRDLYDDDDKLACGGSPAADSTPDGPVQQLPKGEPETDLNPELPAHLIGA
WMSGQGLSWEASQEEAFLRSGAQFSPTHGLALPQDGVYYLYCHVGYRGRTPPAGRSRARS�TLRSALY
RAGGAYGRGSPELLLEGAETVTPVVDPIGYGSLWYTSVGFGGLAQLRSGERVYVNISHPDMVDYRRGKT
FFGAVMVG

291:

his-myc-EK-C-LT• 49-306: SEQ ID NO:291

APLVHHHHHHGPLVDVASNEQKLISEEDLASMTGGQQMGRDLYDDDDKLACGGQDQGRRVEKIIGSGAQ
AQKRLDDSKPSCILPSPSSLSETPDPRHPQRSNASRNLASTSQGPVAQSSREASAWMTILSPAADSTPDGPV
QQLPKGEPETDLNPELPAHLIGAWMSGQGLSWEASQEEAFLRSGAQFSPTHGLALPQDGVYYLYCHVGY
RGRTPPAGRSRARS�TLRSALYRAGGAYGRGSPELLLEGAETVTPVVDPIGYGSLWYTSVGFGGLAQLRSG
ERVYVNISHPDMVDYRRGKTFFGAVMVG

292:

his-myc-EK-C-LT• 126-306: SEQ ID NO:292

APLVHHHHHHGPLVDVASNEQKLISEEDLASMTGGQQMGRDLYDDDDKLACGGSPAADSTPDGPVQQLP
KGEPETDLNPELPAHLIGAWMSGQGLSWEASQEEAFLRSGAQFSPTHGLALPQDGVYYLYCHVGYRGR
PPAGRSRARS�TLRSALYRAGGAYGRGSPELLLEGAETVTPVVDPIGYGSLWYTSVGFGGLAQLRSGERVY
VNISHPDMVDYRRGKTFFGAVMVG

293:

primerMCS-1F

5'-TAT GGA TCC GGC TAG CGC TCG AGG GTT TAA ACG GCG GCC GCA T-3' (SEQ ID NO:293)

294:

primerMCS-1R

5'-TCG AAT GCG GCC GCC GTT TAA ACC CTC GAG CGC TAG CCG GAT CCA-3' (SEQ ID NO:294)

295:

Bamhis6-EK-Nhe-F

5'-GAT CCA CAC CAC CAC CAC CAC GGT TCT GGT GAC GAC GAT GAC AAA GCG CTA GCC C-3'
(SEQ ID NO:295)

20250502 01:30:20

296:

Bamhis6-EK-Nhe-R

5'-TCG AGG GCT AGC GCT TTG TCA TCG TCG TCA CCA GAA CCG TGG TGG TGG TGG TGG TGT G-3'
(SEQ ID NO:296)

297:

oligo1F-C-glycine-linker

5'-TCG AGG GTG GTG GTG GTG GTT GCG GTT AAT AAG TTT AAA CGC-3' (SEQ ID NO:297)

298:

oligo1R-C-glycine-linker

5'-GGC CGC GTT TAA ACT TAT TAA CCG CAA CCA CCA CCA CCA CCC-3' (SEQ ID NO:298)

299:

oligo1F-C-gamma1-linker

5'-TCG AGG ATA AAA CCC ACA CCT CTC CGC CGT GTG GTT AAT AAG TTT AAA CGC-3' (SEQ ID NO:299)

300:

oligo1R-C-gamma1-linker

5'-GGC CGC GTT TAA ACT TAT TAA CCA CAC GGC GGA GAG GTG TGG GTT TTA TCC-3' (SEQ ID NO:300)

301:

oligo1FA-C-gamma3-linker

5'-TCG AGC CGA AAC CGT CTA CCC CGC CGG GTT CTT CTG-3' (SEQ ID NO:301)

302:

oligo1RA-C-gamma3-linker

5'-CAC CAC CAG AAG AAC CCG GCG GGG TAG ACG GTT TCG GC-3' (SEQ ID NO:302)

20250902 10050902

303:

oligo2FB-C-gamma3-linker

5'-GTG GTG CTC CGG GTG GTT GCG GTT AAT AAG TTT AAA CGC-3' (SEQ ID NO:303)

304:

oligo2RB-C-gamma3-linker

5'-GGC CGC GTT TAA ACT TAT TAA CCG CAA CCA CCC GGA G-3' (SEQ ID NO:304)

305:

rMIF-F

5'-GGA ATT CCA TAT GCC TAT GTT CAT CGT GAA CAC-3' (SEQ ID NO:305)

306:

rMIF-Xho-R

5'-CCC GCT CGA GAG CGA AGG TGG AAC CGT TC-3' (SEQ ID NO:306)

307:

rMIF-C1:

MPMFIVNTNVPRASVPEGFLSELTQQLAQATGKPAQYIAVHVVPDQLMTFSGTSDPCALCSLHSIGKIGGAQ
NRNYSKLLCGLLSDRLHISPDRVYINYYDMNAANVGWNGSTFALEGGGGGCG (SEQ ID NO:307)

308:

rMIF-C2

MPMFIVNTNVPRASVPEGFLSELTQQLAQATGKPAQYIAVHVVPDQLMTFSGTSDPCALCSLHSIGKIGGAQ
NRNYSKLLCGLLSDRLHISPDRVYINYYDMNAANVGWNGSTFALEDKTHTSPPCG (SEQ ID NO:308)

309:

rMIF-C3

MPMFIVNTNVPRASVPEGFLSELTQQLAQATGKPAQYIAVHVVPDQLMTFSGTSDPCALCSLHSIGKIGGAQ
NRNYSKLLCGLLSDRLHISPDRVYINYYDMNAANVGWNGSTFALEPKPSTPPGSSGGAPGGCG (SEQ ID
NO:309)

10050902-011302

310:

met-human-MIF-C1

MPMFIVNTNVP RASVPDGFLS ELTQQLAQAT GKPPQYIAVH VVPDQLMAFG GSSEPCALCS
LHSIGKIGGA QNRSYSKLLC GLLAERLRIS PDRVYINYD MNAANVGWNN STFALEGGGGGCG

311:

human-MIF-C1 (SEQ ID NO:311)

PMFIVNTNVP RASVPDGFLS ELTQQLAQAT GKPPQYIAVH VVPDQLMAFG GSSEPCALCS
LHSIGKIGGA QNRSYSKLLC GLLAERLRIS PDRVYINYD MNAANVGWNN STFALEGGGGGCG

312:

met-human-MIF-C2 (SEQ ID NO:312)

MPMFIVNTNVP RASVPDGFLS ELTQQLAQAT GKPPQYIAVH VVPDQLMAFG GSSEPCALCS
LHSIGKIGGA QNRSYSKLLC GLLAERLRIS PDRVYINYD MNAANVGWNN STFALEDKTHTSPPCG

313:

human-MIF-C2 (SEQ ID NO:313)

PMFIVNTNVP RASVPDGFLS ELTQQLAQAT GKPPQYIAVH VVPDQLMAFG GSSEPCALCS
LHSIGKIGGA QNRSYSKLLC GLLAERLRIS PDRVYINYD MNAANVGWNN STFALEDKTHTSPPCG

314:

met-human-MIF-C3 (SEQ ID NO:314)

MPMFIVNTNVP RASVPDGFLS ELTQQLAQAT GKPPQYIAVH VVPDQLMAFG GSSEPCALCS
LHSIGKIGGA QNRSYSKLLCGLLAERLRISPDRVYINYD MNAANVGWNN STFALEPKPSTPPGSSGGAPGGCG

315:

human-MIF-C3 (SEQ ID NO:315)

PMFIVNTNVP RASVPDGFLS ELTQQLAQAT GKPPQYIAVH VVPDQLMAFG GSSEPCALCS
LHSIGKIGGA QNRSYSKLLCGLLAERLRISPDRVYINYD MNAANVGWNN STFALEPKPSTPPGSSGGAPGGCG

316:

RANKL-UP:

5'CTGCCAGGGGCCCCGGGTGCGGCGGTGGCCATCATCACCACCATCACCAGCGCTTCTCAGGAG-3'

317:

RANKL-DOWN :

2009-10-20 09:02:01

5'-CCGCTCGAGTTAGTCTATGTCCTGAACTTTGAAAG-3'

318 and 319:

Protein sequence of GST-PS-C-RANKL (SEQ ID NO:318; capital letters)

cDNA sequence of GST-PS-C-RANKL (SEQ ID NO:319; small letters)

1 M S P I L G Y W K I K G L V Q P T R L L L E Y L E
1 atgtcccctatactaggttattggaaaattaagggccttggtgcaaccactcgacttcttttggaatatcttgaa
26 E K Y E E H L Y E R D E G D K W R N K K F E L G L
76 gaaaaatatgaagagcatttgtatgagcgcatgaaggtgataaatggcgaaacaaaaagtttgaattgggtttg
51 E F P N L P Y Y I D G D V K L T Q S M A I I R Y I
151 gagtttcccaatcttcttattatattgatggtgatgttaaattaacacagtctatggccatcatacgttatata
76 A D K H N M L G G C P K E R A E I S M L E G A V L
226 gctgacaagcacaacatgttgggtggttgtccaaaagagcgtgcagagatttcaatgcttgaaggagcggttttg
101 D I R Y G V S R I A Y S K D F E T L K V D F L S K
301 gatattagatacgggtgtttcgagaattgcatatagtaaagactttgaaactctcaaagttgattttcttagcaag
126 L P E M L K M F E D R L C H K T Y L N G D H V T H
376 ctacctgaaatgctgaaaatgttcgaagatcggttatgtcataaaacatatattaatggtgatcatgtaacccat
151 P D F M L Y D A L D V V L Y M D P M C L D A F P K
451 cctgacttcatgttgtatgacgctcttgatgttgtttttatatacatggaccaatgtgcctggatgcgttcccaaaa
176 L V C F K K R I E A I P Q I D K Y L K S S K Y I A
526 ttatgttgttttaaaaaacgtattgaagctatcccacaaattgataagtaacttgaatccagcaagtatatagca
201 W P L Q G W Q A T F G G G D H P P K S D L E V L F
601 tggccttttgcagggtggcaagccacgtttgggtgggtggcgaccatcctccaaaatcggatctggaagttctgttc
226 Q G P G C G G G H H H H H Q R F S G A P A M M E
676 cagGGGCGGGTGGCGGGTGCCATCATCACCACCATCACCAGCGCTTCTCAGGAGCTCCAGCTATGATGGAA
251 G S W L D V A Q R G K P E A Q P F A H L T I N A A
751 GGCTCATGGTGGATGTGGCCCGAGGCAAGCCTGAGGCCAGCCATTGACACCTCACCATCAATGTGCGC
276 S I P S G S H K V T L S S W Y H D R G W A K I S N
826 AGCATCCCATCGGGTTCCTATAAGTCACTCTGTCTCTTGGTACCACGATCGAGGCTGGGCCAAGATCTCTAAC
301 M T L S N G K L R V N Q D G F Y Y L Y A N I C F R
901 ATGACGTTAAGCAACGGAAGAACTAAGGGTTAACCAAGATGGCTTCTATTACCTGTACGCCAACATTGCTTTTCGG
326 H H E T S G S V P T D Y L Q L M V Y V V K T S I K
976 CATCATGAAACATCGGGAAGCGTACCTACAGACTATCTTCAGCTGATGGTGTATGTCGTTAAACAGCATCAAA
351 I P S S H N L M K G G S T K N W S G N S E F H F Y
1051 ATCCCAAGTTCTCATAACCTGATGAAAGGAGGAGCACGAAAACTGGTCGGGCAATTCTGAATTCCACTTTTAT
376 S I N V G G F F K L R A G E E I S I Q V S N P S L
1126 TCCATAAATGTTGGGGGATTTTCAAGCTCCGAGCTGGTGAAGAAATAGCATTAGGTGTCCAACCTTCCCTG
401 L D P D Q D T Y F G A F K V Q D I D *
1201 CTGGATCCGATCAAGATGCGACGTACTTTGGGGCTTTCAAAGTTTCAGGACATAGACTAACTCGAGCGG

320:

Human-C-RANKL

CGGGQHIRAEKAMVDGSWLDLAKRSKLEAQPFHAHLTINATDIPSGSHKVSLSWYHDRGWAKISNMFTSNGKLI
VNQDGFYYLYANICFRHHETSGDLATEYLQLMVYVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFK
LRSGEEISIEVSNPSLLDPDQDATYFGAFKVRDID

321:

Primer 5'PrP-BamHI

5'-CGG GAT CCC ACC ATG GTG GGG GGC CTT GG -3' (SEQ ID NO:321)

322:

Primer 3'PrP-NheI

5'-CTA GCT AGC CTG GAT CTT CTC CCG -3' (SEQ ID NO:322)

323:

Protein sequence of mPrP_E-EK-Fc*

MVGGLGGYMLGSAMSRPMIHFGNDWEDRYRENMYRYPNQVYYRPVDQYSNQNNFVHDCVNITIKQHT
VTTTTKGENFTETDVKMMERVVEQMCVTQYQKESQAYYDGRSRLAGGGGCGDDDDKLTHTCPPCPAPEA
EGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPASIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPS
DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPG
K

324:

mPrP_E

MVGGLGGYMLGSAMSRPMIHFGNDWEDRYRENMYRYPNQVYYRPVDQYSNQNNFVHDCVNITIKQHT
VTTTTKGENFTETDVKMMERVVEQMCVTQYQKESQAYYDGRSRLAGGGGCGDDDDK

325:

human resistin-C-Xa: (SEQ ID NO:325)

SSKTLCSMEEAINERIQEVAGSLIFRAISSIGLECQSVTSRGDL
ATCPRGFAVTGCTCGSACGSWDVRAETTCHCQCAGMDWTGARCCRVQPGGGGCG
IEGR

326:

human resistin-C-EK: (SEQ ID NO:326)

SSKTLCSMEEAINERIQEVAGSLIFRAISSIGLECQSVTSRGDL
ATCPRGFAVTGCTCGSACGSWDVRAETTCHCQCAGMDWTGARCCRVQPGGGGCG
DDDDK

327:

human resistin-C: (SEQ ID NO:327)

SSKTLCSMEEAINERIQEVAGSLIFRAISSIGLECQSVTSRGDL
ATCPRGFAVTGCTCGSACGSWDVRAETTCHCQCAGMDWTGARCCRVQPGGGGCG

328:

20250902 011802

mouse C-IL-13-F: (SEQ ID NO:328)

ADPGCGGGGGLAGPVPRSVSLPLTLKELIEELSNITQDQTPLCNGSMVWSVDLAAGGFCVALDSLTNISNCN
AIYRTQRILHGLCNRKAPTTVSSLPTKIEVAHFITKLLSYTKQLFRHGPFLEVLAIEGR
329:

mouse C-IL-13-S: (SEQ ID NO:329)

LACGGGGGGPVPRSVSLPLTLKELIEELSNITQDQTPLCNGSMVWSVDLAAGGFCVALDSLTNISNCNAI
YRTQRILHGLCNRKAPTTVSSLPTKIEVAHFITKLLSYTKQLFRHGPF

330:

human C-IL-13-F: (SEQ ID NO:330)

ADPGCGGGGGLAGPVPPSTALRELIEELVNITQNQKAPLCNGSMVWSINLTAGMYCAALESLINVSGCS
AIEKTQRMLSGFCPHKVSAGQFSSLHVRDTKIEVAQFVKDLLHLKKLFREGRFNLEVLAIEGR

331:

human C-IL-13-S: (SEQ ID NO:331)

LACGGGGGGPVPPSTALRELIEELVNITQNQKAPLCNGSMVWSINLTAGMYCAALESLINVSGCSAIEKTQR
MLSGFCPHKVSAGQFSSLHVRDTKIEVAQFVKDLLHLKKLFREGRFN

332:

mouse C-IL-5-E: (SEQ ID NO:332)

ALVCGGPKPSTPPGSSGGAPASMEIPMSTVVKETLTQLSAHRALLTSNETMRLPVPTHKNHQLCIGEIFQG
LDILKNQTVRGGTVEMLFQNLSLIKKYIDRQKEKCGEERRRTRQFLDYLQEFLGVMSTEWAMEG

333:

mouse C-IL-5-F: (SEQ ID NO:333)

ADPGCGGGGGLAMEIPMSTVVKETLTQLSAHRALLTSNETMRLPVPTHKNHQLCIGEIFQGLDILKNQTVR
GGTVEMLFQNLSLIKKYIDRQKEKCGEERRRTRQFLDYLQEFLGVMSTEWAMEGLEVLAIEGR

334:

mouse C-IL-5-S: (SEQ ID NO:334)

LACGGGGGMEIPMSTVVKETLTQLSAHRALLTSNETMRLPVPTHKNHQLCIGEIFQGLDILKNQTVRGG
TVEMLFQNLSLIKKYIDRQKEKCGEERRRTRQFLDYLQEFLGVMSTEWAMEG

335:

human C-IL-5-E: (SEQ ID NO:335)

ALVCGGPKPSTPPGSSGGAPASIPTEIPTALVKETLALLSTHRTLLIANETLRIPVPVHKNHQLCTEEIFQGI
GTLESQTVQGGTVERLFKNLSLIKKYIDGQKKKCGEERRRVNQFLDYLQEFLGVMNTEW IIES

336:

human C-IL-5-F: (SEQ ID NO:336)

10050902.01302

ADPGCGGGGGLAIPTEIPTSALVKETLALLSTHRTLLIANETLRIPVPVHKNHQLCTEEIFQGIGTLESQTVQGG
GTVERLFKNLSLIKKYIDGQKKKCGEERRRVNQFLDYLQEFLGVMNTEW IIES LEVLAIEGR

337:

human C-IL-5-S: (SEQ ID NO:337)

LACGGGGGIPTEIPTSALVKETLALLSTHRTLLIANETLRIPVPVHKNHQLCTEEIFQGIGTLESQTVQGGT
VERLFKNLSLIKKYIDGQKKKCGEERRRVNQFLDYLQEFLGVMNTEW IIES

338:

primer NheIL13-F: (SEQ ID NO:338)

CTAGCTAGCCGGGCCGGTGCCAAGATC

339:

primer XhoIL13-R: (SEQ ID NO:339)

TTTCTCGAGGAAGGGGCCGTGGCGAA

340:

primer Spelinker3-F1: (SEQ ID NO:340)

CCCCGCCGGGTTCTTCTGGCGGTGCTCCGGCTAGCATGGAGATTCCCATGAGCAC

341:

Primer SpeNlinker3-F2: (SEQ ID NO:341)

TTTTACTAGTTGGTTGCGGCGGCCCGAAACCGAGCACCCCGCCGGGTTCTTC

342:

Primer IL5StopXho-R: (SEQ ID NO:342)

TTTTGCGGCCGCGTTTAAACTCGAGTTATTAGCCTTCCATTGCCCACTC

343:

Primer BamH1-FLK1-F: (SEQ ID NO:343)

CGCGGATCCATTCATCGCCTCTGTC

344:

Primer Nhe1-FLK1-B: (SEQ ID NO:344)

CTAGCTAGCTTTGTGTGAACTCGGAC

345:

mVEGFR-2 (2-3) fragment: (SEQ ID NO:345)

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PFIAS VSDQHGIYVI TENKNKTVVI PCRGSISNLN VSLCARYPEK RFVPDGNRIS WDSEIGFTLP
SYMISYAGMV FCEAKINDET YQSIMYIVVV VGYRIYDVIL SPPHEIELSA GEKLVNLCTA
RTELNVGLDF TWHSPPSKSH HKKIVNRDVK PFPGTVAKMF LSTLTIESVT KSDQGEYTCV
ASSGRMIKRN RTFVRVHTKP

346

human C-LT• 49-306 : (SEQ ID NO:346)

LACGGQDQGRRVEKIIGSGAQAQKRLDDSKPSCILPSPSSLSETPDPRLHPQRSNASRNLASTSQGPVAQSSR
EASAWMTILSPAADSTPDPGVQQLPKGEPETDLNPELPAAHLIGAWMSGQGLSWEASQEEAFLRSGAQFSP
THGLALPDGVIYLYCHVGYRGRTPPAGRSRARSLLRSALYRAGGAYGRGSPPELLLEGAETVTPVVDPIG
YGSLWYTSVGFGLAQLRSGERVYVNISHPDMVDYRRGKTFFGAVMVG

347

human C-LT• 126-306 : (SEQ ID NO:347)

LACGGSPAADSTPDPGVQQLPKGEPETDLNPELPAAHLIGAWMSGQGLSWEASQEEAFLRSGAQFSPHGL
ALPDGVIYLYCHVGYRGRTPPAGRSRARSLLRSALYRAGGAYGRGSPPELLLEGAETVTPVVDPIGYGSL
WYTSVGFGLAQLRSGERVYVNISHPDMVDYRRGKTFFGAVMVG

348

Modified human prion protein fragment: (SEQ ID NO:348)

VGGLGGYMLGSAMSRPIHFGSDYEDRYRENMHRYPNQVYYRPMDE
YSNQNNFVHDCVNITIKQHTVTTTTKGENFTETDVKMMERVVEQMCITQYQRESQAYYQ
RGRLAGGGGCG

349

Modified bovine prion protein fragment: (SEQ ID NO:349)

VGGLGGYMLGSAMSRPLIHFGSDYEDRYRENMHRYPNQVYYRPVDQ
YSNQNNFVHDCVNITVKEHTVTTTTKGENFTETDIKMMERVVEQMCITQYQRESQAYYQ
RGRLAGGGGCG

350

Modified sheep prion protein fragment: (SEQ ID NO:350)

VGGLGGYMLGSAMSRPLIHFGNDYEDRYRENMYRYPNQVYYRPVDR
YSNQNNFVHDCVNITVKQHTVTTTTKGENFTETDIKIMERVVEQMCITQYQRESQAYYQ
RGRLAGGGGCG

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